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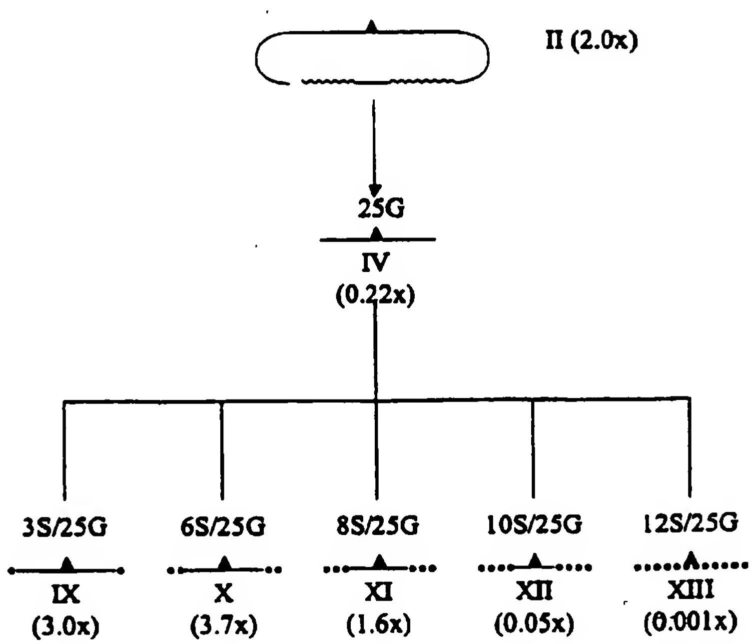
(54) **Title:** TARGETED CHROMOSOMAL GENOMIC ALTERATIONS WITH MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES



(57) **Abstract:** Presented are methods and compositions for targeted chromosomal genomic alterations using modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified single-stranded oligonucleotides. The oligonucleotides of the invention have at least one modified nuclease-resistant terminal region comprising phophorothioate linkages, LNA analogs or 2'-O-Me base analogs.

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TARGETED CHROMOSOMAL GENOMIC ALTERATIONS WITH MODIFIED SINGLE STRANDED OLIGONUCLEOTIDES

Field Of The Invention

The technical field of the invention is oligonucleotide-directed repair or alteration of genetic information using novel chemically modified oligonucleotides. Such genetic information is preferably from a eukaryotic organism, i.e. a plant, animal or fungus.

Background Of The Invention

A number of methods have been developed specifically to alter the sequence of an isolated DNA in addition to methods to alter directly the genomic information of various plants, fungi and animals, including humans ("gene therapy"). The latter methods generally include the use of viral or plasmid vectors carrying nucleic acid sequences encoding partial or complete portions of a particular protein which is expressed in a cell or tissue to effect the alteration. The expression of the particular protein then results in the desired phenotype. For example, retroviral vectors containing a transgenic DNA sequence allowing for the production of a normal CFTR protein when administered to defective cells are described in U.S. Patent 5,240,846. Others have developed different "gene therapy vectors" which include, for example, portions of adenovirus (Ad) or adeno-associated virus (AAV), or other viruses. The virus portions used are often long terminal repeat sequences which are added to the ends of a transgene of choice along with other necessary control sequences which allow expression of the transgene. See U.S. Patents 5,700,470 and 5,139,941. Similar methods have been developed for use in plants. See, for example, U.S. Patent 4,459,355 which describes a method for transforming plants with a DNA vector and U.S. Patent 5,188,642 which describes cloning or expression vectors containing a transgenic DNA sequence which when expressed in plants confers resistance to the herbicide glyphosate. The use of such transgene vectors in any eukaryotic organism adds one or more exogenous copies of a gene, which gene may be foreign to the host, in a usually random fashion at one or more integration sites of the organism's genome at some frequency. The gene which was originally present in the genome, which may be a normal allelic variant, mutated, defective, and/or functional, is retained in the genome of the host.

These methods of gene correction are problematic in that complications which can compromise the health of the recipient, or even lead to death, may result. One such problem is that insertion of exogenous nucleic acid at random location(s) in the genome can have deleterious effects. Another problem with such systems includes the addition of unnecessary and unwanted genetic material to the genome of the recipient, including, for example, viral or other vector remnants, control sequences required to allow production of the transgene protein, and reporter genes or resistance markers. Such remnants and added sequences may have presently unrecognized consequences, for example, involving genetic rearrangements of the recipient genomes. Other problems associated with these types of traditional gene therapy methods include autoimmune suppression of cells expressing an inserted gene due to the presence of foreign antigens. Concerns have also been raised with consumption, especially by humans, of plants containing exogenous genetic material.

More recently, simpler systems involving poly- or oligo- nucleotides have been described for use in the alteration of genomic DNA. These chimeric RNA-DNA oligonucleotides, requiring contiguous RNA and DNA bases in a double-stranded molecule folded by complementarity into a double hairpin conformation, have been shown to effect single basepair or frameshift alterations, for example, for mutation or repair of plant or animal genomes. See, for example, WO 99/07865 and U.S. Patent 5,565,350. In the chimeric RNA-DNA oligonucleotide, an uninterrupted stretch of DNA bases within the molecule is required for sequence alteration of the targeted genome while the obligate RNA residues are involved in complex stability. Due to the length, backbone composition, and structural configuration of these chimeric RNA-DNA molecules, they are expensive to synthesize and difficult to purify. Moreover, if the RNA-containing strand of the chimeric RNA-DNA oligonucleotide is designed so as to direct gene conversion, a series of mutagenic reactions resulting in nonspecific base alteration can result. Such a result compromises the utility of such a molecule in methods designed to alter the genomes of plants and animals, including in human gene therapy applications.

Alternatively, other oligo- or poly- nucleotides have been used which require a triplex forming, usually polypurine or polypyrimidine, structural domain which binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. Such oligonucleotides may have an additional DNA reactive moiety, such as psoralen, covalently linked to the oligonucleotide. These reactive moieties function as effective intercalation agents, stabilize the formation of a triplex and can be mutagenic. Such agents may be required in order to stabilize the triplex forming domain of the oligonucleotide with the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. The utility of

these oligonucleotides for directing gene conversion is compromised by a high frequency of nonspecific base changes.

In more recent work, the domain for altering a genome is linked or tethered to the triplex forming domain of the bi-functional oligonucleotide, adding an additional linking or tethering functional domain to the oligonucleotide. See, e.g., Culver et al., Nature Biotechnology 17: 989-93 (1999). Such chimeric or triplex forming molecules have distinct structural requirements for each of the different domains of the complete poly- or oligo-nucleotide in order to effect the desired genomic alteration in either episomal or chromosomal targets.

Other genes, e.g. CFTR, have been targeted by homologous recombination using duplex fragments having several hundred basepairs. See, e.g., Kunzelmann et al., Gene Ther. 3:859-867 (1996). Early experiments to mutagenize an antibiotic resistance indicator gene by homologous recombination used an unmodified DNA oligonucleotide with no functional domains other than a region of complementary sequence to the target. See Campbell et al., New Biologist 1: 223-227 (1989). These experiments required large concentrations of the oligonucleotide, exhibited a very low frequency of episomal modification of a targeted exogenous plasmid gene not normally found in the cell and have not been reproduced. However, as shown in the examples herein, we have observed that an unmodified DNA oligonucleotide can convert a base at low frequency which is detectable using the assay systems described herein.

Artificial chromosomes can be useful for the screening purposed identified herein. These molecules are man-made linear or circular DNA molecules constructed from essential cis-acting DNA sequence elements that are responsible for the proper replication and partitioning of natural chromosomes (Murray et al., 1983). The essential elements are: (1) Autonomous Replication Sequences (ARS), (2) Centromeres, and (3) Telomeres.

Yeast artificial chromosomes (YACs) allow large genomic DNA to be modified and used for generating transgenic animals [Burke et al., Science 236:806; Peterson et al., Trends Genet. 13:61 (1997); Choi, et al., Nat. Genet., 4:117-223 (1993), Davies, et al., Biotechnology 11:911-914 (1993), Matsuura, et al., Hum. Mol. Genet., 5:451-459 (1996), Peterson et al., Proc. Natl. Acad. Sci., 93:6605-6609 (1996); and Schedl, et al., Cell, 86:71-82 (1996)]. Other vectors also have been developed for the cloning of large segments of mammalian DNA, including cosmids, and bacteriophage P1 [Sternberg et al., Proc. Natl. Acad. Sci. U.S.A., 87:103-107 (1990)]. YACs have certain advantages over these alternative large capacity cloning vectors [Burke et al., Science, 236:806-812 (1987)]. The

maximum insert size is 35-30 kb for cosmids, and 100 kb for bacteriophage P1, both of which are much smaller than the maximal insert for a YAC.

An alternative to YACs are E. coli based cloning systems based on the E. coli fertility factor that have been developed to construct large genomic DNA insert libraries. They are bacterial artificial chromosomes (BACs) and P-1 derived artificial chromosomes (PACs) [Mejia et al., Genome Res. 7:179-186 (1997); Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Ioannou et al., Nat. Genet., 6:84-89 (1994); Hosoda et al., Nucleic Acids Res. 18:3863 (1990)]. BACs are based on the E. coli fertility plasmid (F factor); and PACs are based on the bacteriophage P1. These vectors propagate at a very low copy number (1-2 per cell) enabling genomic inserts up to 300 kb in size to be stably maintained in recombination deficient hosts. Furthermore, the PACs and BACs are circular DNA molecules that are readily isolated from the host genomic background by classical alkaline lysis [Birnboim et al., Nucleic Acids Res. 7:1513-1523 (1979].

Oligonucleotides designed for use in the alteration of genetic information are significantly different from oligonucleotides designed for antisense approaches. For example, antisense oligonucleotides are perfectly complementary to and bind an mRNA strand in order to modify expression of a targeted mRNA and are used at high concentration. As a consequence, they are unable to produce a gene conversion event by either mutagenesis or repair of a defect in the chromosomal DNA of a host genome. Furthermore, the backbone chemical composition used in most oligonucleotides designed for use in antisense approaches renders them inactive as substrates for homologous pairing or mismatch repair enzymes and the high concentrations of oligonucleotide required for antisense applications can be toxic with some types of nucleotide modifications. In addition, antisense oligonucleotides must be complementary to the mRNA and therefore, may not be complementary to the other DNA strand or to genomic sequences that span the junction between intron sequence and exon sequence.

A need exists for simple, inexpensive oligonucleotides capable of producing targeted alteration of genetic material such as those described herein as well as methods to identify optimal oligonucleotides that accurately and efficiently alter target DNA.

Summary Of The Invention

Novel, modified single-stranded nucleic acid molecules that direct gene alteration in plants, fungi and animals are identified and the efficiency of alteration is analyzed both in vitro using a cell-free extract assay and in vivo using a yeast cell system. The alteration in an oligonucleotide of the invention may comprise an insertion, deletion, substitution, as well as any combination of these. Site

specific alteration of DNA is not only useful for studying function of proteins in vivo, but it is also useful for creating animal models for human disease, and in gene therapy. As described herein, oligonucleotides of the invention target directed specific gene alterations in genomic double-stranded DNA cells. The target DNA can be normal, cellular chromosomal DNA, extrachromosomal DNA present in cells in different forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), as well as episomal DNA, including episomal DNA from an exogenous source such as a plasmid or recombinant vector. Many of these artificial chromosome constructs containing human DNA can be obtained from a variety of sources, including, e.g., the Whitehead Institute, and are described, e.g., in Cohen et al., Nature 336:698-701 (1993) and Chumakov, et al., Nature 377:174-297 (1995). The target DNA may be transcriptionally silent or active. In a preferred embodiment, the target DNA to be altered is the non-transcribed strand of a genomic DNA duplex.

The low efficiency of gene alteration obtained using unmodified DNA oligonucleotides is believed to be largely the result of degradation by nucleases present in the reaction mixture or the target cell. Although different modifications are known to have different effects on the nuclease resistance of oligonucleotides or stability of duplexes formed by such oligonucleotides (see, e.g., Koshkin et al., J. Am. Chem. Soc., 120:13252-3), we have found that it is not possible to predict which of any particular known modification would be most useful for any given alteration event, including for the construction of gene conversion oligonucleotides, because of the interaction of different as yet unidentified proteins during the gene alteration event. Herein, a variety of nucleic acid analogs have been developed that increase the nuclease resistance of oligonucleotides that contain them, including, e.g., nucleotides containing phosphorothioate linkages or 2'-O-methyl analogs. We recently discovered that single-stranded DNA oligonucleotides modified to contain 2'-O-methyl RNA nucleotides or phosphorothioate linkages can enable specific alteration of genetic information at a higher level than either unmodified single-stranded DNA or a chimeric RNA/DNA molecule. See priority applications incorporated herein in their entirety; see also Gamper et al., Nucleic Acids Research 28: 4332-4339 (2000). We also found that additional nucleic acid analogs which increase the nuclease resistance of oligonucleotides that contain them, including, e.g., "locked nucleic acids" or "LNAs", xylo-LNAs and L-ribo-LNAs; see, for example, Wengel & Nielsen, WO 99/14226; Wengel, WO 00/56748 and Wengel, WO 00/66604; also allow specific targeted alteration of genetic information.

The assay allows for determining the optimum length of the oligonucleotide, optimum sequence of the oligonucleotide, optimum position of the mismatched base or bases, optimum chemical

modification or modifications, optimum strand targeted for identifying and selecting the most efficient oligonucleotide for a particular gene alteration event by comparing to a control oligonucleotide. Control oligonucleotides may include a chimeric RNA-DNA double hairpin oligonucleotide directing the same gene alteration event, an oligonucleotide that matches its target completely, an oligonucleotide in which all linkages are phosphorothiolated, an oligonucleotide fully substituted with 2'-O-methyl analogs or an RNA oligonucleotide. Such control oligonucleotides either fail to direct a targeted alteration or do so at a lower efficiency as compared to the oligonucleotides of the invention. The assay further allows for determining the optimum position of a gene alteration event within an oligonucleotide, optimum concentration of the selected oligonucleotide for maximum alteration efficiency by systematically testing a range of concentrations, as well as optimization of either the source of cell extract by testing different organisms or strains, or testing cells derived from different organisms or strains, or cell lines. Using a series of single-stranded oligonucleotides, comprising all RNA or DNA residues and various mixtures of the two, several new structures are identified as viable molecules in nucleotide conversion to direct or repair a genomic mutagenic event. When extracts from mammalian, plant and fungal cells are used and are analyzed using a genetic readout assay in bacteria, single-stranded oligonucleotides having one of several modifications are found to be more active than a control RNA-DNA double hairpin chimera structure when evaluated using an in vitro gene repair assay. Similar results are also observed in vivo using yeast, mammalian, rodent, monkey, human and embryonic cells, including stem cells. Molecules containing various lengths of modified bases were found to possess greater activity than unmodified single-stranded DNA molecules.

Detailed Description Of The Invention

The present invention provides oligonucleotides having chemically modified, nuclease resistant residues, preferably at or near the termini of the oligonucleotides, and methods for their identification and use in targeted alteration of genetic material, including gene mutation, targeted gene repair and gene knockout. The oligonucleotides are preferably used for mismatch repair or alteration by changing at least one nucleic acid base, or for frameshift repair or alteration by addition or deletion of at least one nucleic acid base. The oligonucleotides of the invention direct any such alteration, including gene correction, gene repair or gene mutation and can be used, for example, to introduce a polymorphism or haplotype or to eliminate ("knockout") a particular protein activity.

The oligonucleotides of the invention are designed as substrates for homologous pairing and repair enzymes and as such have a unique backbone composition that differs from chimeric RNA-

DNA double hairpin oligonucleotides, antisense oligonucleotides, and/or other poly- or oligo-nucleotides used for altering genomic DNA, such as triplex forming oligonucleotides. The single-stranded oligo-nucleotides described herein are inexpensive to synthesize and easy to purify. In side-by-side comparisons, an optimized single-stranded oligonucleotide comprising modified residues as described herein is significantly more efficient than a chimeric RNA-DNA double hairpin oligonucleotide in directing a base substitution or frameshift mutation in a cell-free extract assay.

We have discovered that single-stranded oligonucleotides having a DNA domain surrounding the targeted base, with the domain preferably central to the poly- or oligo-nucleotide, and having at least one modified end, preferably at the 3' terminal region are able to alter a target genetic sequence and with an efficiency that is higher than chimeric RNA-DNA double hairpin oligonucleotides disclosed in US Patent 5,565,350. Oligonucleotides of the invention can efficiently be used to introduce targeted alterations in a genetic sequence of DNA in the presence of human, animal, plant, fungal (including yeast) proteins and in cultured cells of human liver, lung, colon, cervix, kidney, epethelium and cancer cells and in monkey, hamster, rat and mouse cells of different types, as well as embryonic stem cells. Cells for use in the invention include, e.g., fungi including *S. cerevisiae*, *Ustillago maydis* and *Candida albicans*, mammalian, mouse, hamster, rat, monkey, human and embryonic cells including stem cells. The DNA domain is preferably fully complementary to one strand of the gene target, except for the mismatch base or bases responsible for the gene alteration or conversion events. On either side of the preferably central DNA domain, the contiguous bases may be either RNA bases or, preferably, are primarily DNA bases. The central DNA domain is generally at least 8 nucleotides in length. The base(s) targeted for alteration in the most preferred embodiments are at least about 8, 9 or 10 bases from one end of the oligonucleotide.

According to certain embodiments, the termini of the oligonucleotides of the present invention comprise phosphorothioate modifications, LNA backbone modifications, or 2'-O-methyl base analogs, or any combination of these modifications. Oligonucleotides comprising 2'-O-methyl or LNA analogs are a mixed DNA/RNA polymer. These oligonucleotides are, however, single-stranded and are not designed to form a stable internal duplex structure within the oligonucleotide. The efficiency of gene alteration is surprisingly increased with oligonucleotides having internal complementary sequence comprising phosphorothioate modified bases as compared to 2'-O-methyl modifications. This result indicates that specific chemical interactions are involved between the converting oligonucleotide and the proteins involved in the conversion. The effect of other such chemical interactions to produce nuclease resistant termini using modifications other than LNA, phosphorothioate linkages, or 2'-O-methyl analog

incorporation into an oligonucleotide can not yet be predicted because the proteins involved in the alteration process and their particular chemical interaction with the oligonucleotide substituents are not yet known and cannot be predicted.

In the examples, correcting oligonucleotides of defined sequence are provided for correction of genes mutated in human diseases. In the tables of these examples, the oligonucleotides of the invention are not limited to the particular sequences disclosed. The oligonucleotides of the invention include extensions of the appropriate sequence of the longer 120 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Thus the oligonucleotides of the invention include for each correcting change, oligonucleotides of length 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. Moreover, the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides of the invention as disclosed in the various tables for correction of human diseases contain phosphorothioate linkages, 2'-O-methyl analogs or LNAs or any combination of these modifications just as the assay oligonucleotides do.

The present invention, however, is not limited to oligonucleotides that contain any particular nuclease resistant modification. Oligonucleotides of the invention may be altered with any combination of additional LNAs, phosphorothioate linkages or 2'-O-methyl analogs to maximize conversion efficiency. For oligonucleotides of the invention that are longer than about 17 to about 25 bases in length, internal as well as terminal region segments of the backbone may be altered. Alternatively, simple fold-back structures at each end of a oligonucleotide or appended end groups may be used in addition to a modified backbone for conferring additional nuclease resistance.

The different oligonucleotides of the present invention preferably contain more than one of the aforementioned backbone modifications at each end. In some embodiments, the backbone modifications are adjacent to one another. However, the optimal number and placement of backbone modifications for any individual oligonucleotide will vary with the length of the oligonucleotide and the particular type of backbone modification(s) that are used. If constructs of identical sequence having phosphorothioate linkages are compared, 2, 3, 4, 5, or 6 phosphorothioate linkages at each end are preferred. If constructs of identical sequence having 2'-O-methyl base analogs are compared, 1, 2, 3 or 4

analogs are preferred. The optimal number and type of backbone modifications for any particular oligonucleotide useful for altering target DNA may be determined empirically by comparing the alteration efficiency of the oligonucleotide comprising any combination of the modifications to a control molecule of comparable sequence using any of the assays described herein. The optimal position(s) for oligonucleotide modifications for a maximally efficient altering oligonucleotide can be determined by testing the various modifications as compared to control molecule of comparable sequence in one of the assays disclosed herein. In such assays, a control molecule includes, e.g., a completely 2'-O-methyl substituted molecule, a completely complementary oligonucleotide, or a chimeric RNA-DNA double hairpin.

Increasing the number of phosphorothioate linkages, LNAs or 2'-O-methyl bases beyond the preferred number generally decreases the gene repair activity of a 25 nucleotide long oligonucleotide. Based on analysis of the concentration of oligonucleotide present in the extract after different time periods of incubation, it is believed that the terminal modifications impart nuclease resistance to the oligonucleotide thereby allowing it to survive within the cellular environment. However, this may not be the only possible mechanism by which such modifications confer greater efficiency of conversion. For example, as disclosed herein, certain modifications to oligonucleotides confer a greater improvement to the efficiency of conversion than other modifications.

Efficiency of conversion is defined herein as the percentage of recovered substate molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. the genome of a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be sequenced to determine the percentage that have acquired the desire change. The oligonucleotides of the invention in different embodiments can alter DNA one, two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold more than control oligonucleotides. Such control oligonucleotides are oligonucleotides with fully phosphorothiolated linkages, oligonucleotides that are fully substituted with 2'-O-methyl analogs, a perfectly matched oligonucleotide that is fully complementary to a target sequence or a chimeric DNA-RNA double hairpin oligonucleotide such as disclosed in US Patent 5,565,350.

In addition, for a given oligonucleotide length, additional modifications interfere with the ability of the oligonucleotide to act in concert with the cellular recombination or repair enzyme machinery which is necessary and required to mediate a targeted substitution, addition or deletion event in DNA. For

example, fully phosphorothiolated or fully 2-O-methylated molecules are inefficient in targeted gene alteration.

The oligonucleotides of the invention as optimized for the purpose of targeted alteration of genetic material, including gene knockout or repair, are different in structure from antisense oligonucleotides that may possess a similar mixed chemical composition backbone. The oligonucleotides of the invention differ from such antisense oligonucleotides in chemical composition, structure, sequence, and in their ability to alter genomic DNA. Significantly, antisense oligonucleotides fail to direct targeted gene alteration. The oligonucleotides of the invention may target either the Watson or the Crick strand of DNA and can include any component of the genome including, for example, intron and exon sequences. The preferred embodiment of the invention is a modified oligonucleotide that binds to the non-transcribed strand of a genomic DNA duplex. In other words, the preferred oligonucleotides of the invention target the sense strand of the DNA, i.e. the oligonucleotides of the invention are complementary to the non-transcribed strand of the target duplex DNA. The sequence of the non-transcribed strand of a DNA duplex is found in the mRNA produced from that duplex, given that mRNA uses uracil-containing nucleotides in place of thymine-containing nucleotides.

Moreover, the initial observation that single-stranded oligonucleotides comprising these modifications and lacking any particular triplex forming domain have reproducibly enhanced gene repair activity in a variety of assay systems as compared to a chimeric RNA-DNA double-stranded hairpin control or single-stranded oligonucleotides comprising other backbone modifications was surprising. The single-stranded molecules of the invention totally lack the complementary RNA binding structure that stabilizes a normal chimeric double-stranded hairpin of the type disclosed in U.S. Patent 5,565,350 yet is more effective in producing targeted base conversion as compared to such a chimeric RNA-DNA double-stranded hairpin. In addition, the molecules of the invention lack any particular triplex forming domain involved in Hoogsteen interactions with the DNA double helix and required by other known oligonucleotides in other oligonucleotide dependant gene conversion systems. Although the lack of these functional domains was expected to decrease the efficiency of an alteration in a sequence, just the opposite occurs: the efficiency of sequence alteration using the modified oligonucleotides of the invention is higher than the efficiency of sequence alteration using a chimeric RNA-DNA hairpin targeting the same sequence alteration. Moreover, the efficiency of sequence alteration or gene conversion directed by an unmodified oligonucleotide is many times lower as compared to a control chimeric RNA-DNA molecule or the modified oligonucleotides of the invention targeting the same sequence alteration. Similarly,

molecules containing at least 3 2'-O-methyl base analogs are about four to five fold less efficient as compared to an oligonucleotide having the same number of phosphorothioate linkages.

The oligonucleotides of the present invention for alteration of a single base are about 17 to about 121 nucleotides in length, preferably about 17 to about 74 nucleotides in length. Most preferably, however, the oligonucleotides of the present invention are at least about 25 bases in length, unless there are self-dimerization structures within the oligonucleotide. If the oligonucleotide has such an unfavorable structure, lengths longer than 35 bases are preferred. Oligonucleotides with modified ends both shorter and longer than certain of the exemplified, modified oligonucleotides herein function as gene repair or gene knockout agents and are within the scope of the present invention.

Once an oligomer is chosen, it can be tested for its tendency to self-dimerize, since self-dimerization may result in reduced efficiency of alteration of genetic information. Checking for self-dimerization tendency can be accomplished manually or, more preferably, by using a software program. One such program is Oligo Analyzer 2.0, available through Integrated DNA Technologies (Coralville, IA 52241) (http://www.idtdna.com); this program is available for use on the world wide web at

http://www.idtdna.com/program/oligoanalyzer/
oligoanalyzer.asp.

For each oligonucleotide sequence input into the program, Oligo Analyzer 2.0 reports possible self-dimerized duplex forms, which are usually only partially duplexed, along with the free energy change associated with such self-dimerization. Delta G-values that are negative and large in magnitude, indicating strong self-dimerization potential, are automatically flagged by the software as "bad". Another software program that analyzes oligomers for pair dimer formation is Primer Select from DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715, Phone: (608) 258-7420
(http://www.dnastar.com/products/PrimerSelect.html).
If the sequence is subject to significant self-dimerization, the addition of further sequence flanking the "repair" nucleotide can improve gene correction frequency.

Generally, the oligonucleotides of the present invention are identical in sequence to one strand of the target DNA, which can be either strand of the target DNA, with the exception of one or more targeted bases positioned within the DNA domain of the oligonucleotide, and preferably toward the middle between the modified terminal regions. Preferably, the difference in sequence of the oligonucleotide as compared to the targeted genomic DNA is located at about the middle of the oligonucleotide sequence. In a preferred embodiment, the oligonucleotides of the invention are complementary to the non-transcribed strand of a duplex. In other words, the preferred oligonucleotides target the sense strand of the DNA, i.e.

the oligonucleotides of the invention are preferably complementary to the strand of the target DNA the sequence of which is found in the mRNA.

The oligonucleotides of the invention can include more than a single base change. In an oligonucleotide that is about a 70-mer, with at least one modified residue incorporated on the ends, as disclosed herein, multiple bases can be simultaneously targeted for change. The target bases may be up to 27 nucleotides apart and may not be changed together in all resultant plasmids in all cases. There is a frequency distribution such that the closer the target bases are to each other in the central DNA domain within the oligonucleotides of the invention, the higher the frequency of change in a given cell. Target bases only two nucleotides apart are changed together in every case that has been analyzed. The farther apart the two target bases are, the less frequent the simultaneous change. Thus, oligonucleotides of the invention may be used to repair or alter multiple bases rather than just one single base. For example, in a 74-mer oligonucleotide having a central base targeted for change, a base change event up to about 27 nucleotides away can also be effected. The positions of the altering bases within the oligonucleotide can be optimized using any one of the assays described herein. Preferably, the altering bases are at least about 8 nucleotides from one end of the oligonucleotide.

The oligonucleotides of the present invention can be introduced into cells by any suitable means. According to certain preferred embodiments, the modified oligonucleotides may be used alone. Suitable means, however, include the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, microinjection and other methods known in the art to facilitate cellular uptake. According to certain preferred embodiments of the present invention, the isolated cells are treated in culture according to the methods of the invention, to mutate or repair a target gene. Modified cells may then be reintroduced into the organism as, for example, in bone marrow having a targeted gene. Alternatively, modified cells may be used to regenerate the whole organism as, for example, in a plant having a desired targeted genomic change. In other instances, targeted genomic alteration, including repair or mutagenesis, may take place in vivo following direct administration of the modified, single-stranded oligonucleotides of the invention to a subject.

The single-stranded, modified oligonucleotides of the present invention have numerous applications as gene repair, gene modification, or gene knockout agents. Such oligonucleotides may be advantageously used, for example, to introduce or correct multiple point mutations. Each mutation leads to the addition, deletion or substitution of at least one base pair. The methods of the present invention offer distinct advantages over other methods of altering the genetic makeup of an organism, in that only the individually targeted bases are altered. No additional foreign DNA sequences are added to the

genetic complement of the organism. Such agents may, for example, be used to develop plants or animals with improved traits by rationally changing the sequence of selected genes in cultured cells. Modified cells are then cloned into whole plants or animals having the altered gene. See, e.g., U.S. Patent 6,046,380 and U.S. Patent 5,905,185 incorporated hererin by reference. Such plants or animals produced using the compositions of the invention lack additional undesirable selectable markers or other foreign DNA sequences. Targeted base pair substitution or frameshift mutations introduced by an oligonucleotide in the presence of a cell-free extract also provides a way to modify the sequence of extrachromosomal elements, including, for example, plasmids, cosmids and artificial chromosomes. The oligonucleotides of the invention also simplify the production of transgenic animals having particular modified or inactivated genes. Altered animal or plant model systems such as those produced using the methods and oligonucleotides of the invention are invaluable in determining the function of a gene and in evaluating drugs. The oligonucleotides and methods of the present invention may also be used for gene therapy to correct mutations causative of human diseases.

The purified oligonucleotide compositions may be formulated in accordance with routine procedures as a pharmaceutical composition adapted for bathing cells in culture, for microinjection into cells in culture, and for intravenous administration to human beings or animals. Typically, compositions for cellular administration or for intravenous administration into animals, including humans, are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anaesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients will be supplied either separately or mixed together in unit dosage form, for example, as a dry, lyophilized powder or water-free concentrate. The composition may be stored in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent in activity units. Where the composition is administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade "water for injection" or saline. Where the composition is to be administered by injection, an ampule of sterile water for injection or saline may be provided so that the ingredients may be mixed prior to administration.

Pharmaceutical compositions of this invention comprise the compounds of the present invention and pharmaceutically acceptable salts thereof, with any pharmaceutically acceptable ingredient, excipient, carrier, adjuvant or vehicle.

The oligonucleotides of the invention are preferably administered to the subject in the form of an injectable composition. The composition is preferably administered parenterally, meaning intravenously, intraarterially, intrathecally, interstitially or intracavitarilly. Pharmaceutical compositions of

this invention can be administered to mammals including humans in a manner similar to other diagnostic or therapeutic agents. The dosage to be administered, and the mode of administration will depend on a variety of factors including age, weight, sex, condition of the subject and genetic factors, and will ultimately be decided by medical personnel subsequent to experimental determinations of varying dosage as described herein. In general, dosage required for correction and therapeutic efficacy will range from about 0.001 to 50,000 µg/kg, preferably between 1 to 250 µg/kg of host cell or body mass, and most preferably at a concentration of between 30 and 60 micromolar.

For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In a preferred method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim) or an equivalent such as lipofectin. The amount of the oligonucleotide used is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells. For electroporation, between 20 and 2000 nanograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein.

Another aspect of the invention is a kit comprising at least one oligonucleotide of the invention. The kit may comprise an addition reagent or article of manufacture. The additional reagent or article of manufacture may comprise a cell extract, a cell, or a plasmid, such as one of those disclosed in the Figures herein, for use in an assay of the invention.

Brief Description Of The Drawings

Figure 1. *Flow diagram for the generation of modified single-stranded oligonucleotides.* The upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (A) 2'-O-methyl RNA nucleotides or (B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. HUH7 cells are described in Nakabayashi et al., Cancer Research 42: 3858-3863 (1982). Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene. The numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the molecule. Hence oligo 12S/25G contains an all phosphorothioate backbone, displayed as a dotted line. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA

residues and the carat indicates the mismatched base site (G). Figure 1(C) provides a schematic plasmid indicating the sequence of the kan chimeric double-stranded hairpin oligonucleotide (left) and the sequence the tet chimeric double-stranded hairpin oligonucleotide used in other experiments. Figure 1(D) provides a flow chart of a kan experiment in which a chimeric double-stranded hairpin oligonucleotide is used.

Figure 2. *Genetic readout system for correction of a point mutation in plasmid* pK^{s}m4021. A mutant kanamycin gene harbored in plasmid pK^{s}m4021 is the target for correction by oligonucleotides. The mutant G is converted to a C by the action of the oligo. Corrected plasmids confer resistance to kanamycin in *E.coli* (DH10B) after electroporation leading to the genetic readout and colony counts.

Figure 3: *Target plasmid and sequence correction of a frameshift mutation by chimeric and single-stranded oligonucleotides.* (A) Plasmid pT^{s}Δ208 contains a single base deletion mutation at position 208 rendering it unable to confer tet resistance. The target sequence presented below indicates the insertion of a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) DNA sequence confirming base insertion directed by Tet 3S/25G; the yellow highlight indicates the position of frameshift repair.

Figure 4. *DNA sequences of representative kan^r colonies.* Confirmation of sequence alteration directed by the indicated molecule is presented along with a table outlining codon distribution. Note that 10S/25G and 12S/25G elicit both mixed and unfaithful gene repair. The number of clones sequenced is listed in parentheses next to the designation for the single-stranded oligonucleotide. A plus (+) symbol indicates the codon identified while a figure after the (+) symbol indicates the number of colonies with a particular sequence. TAC/TAG indicates a mixed peak. Representative DNA sequences are presented below the table with yellow highlighting altered residues.

Figure 5. *Gene correction in HeLa cells.* Representative oligonucleotides of the invention are co-transfected with the pCMVneo(⁻)FlAsH plasmid (shown in Figure 9) into HeLa cells. Ligand is diffused into cells after co-transfection of plasmid and oligonucleotides. Green fluorescence indicates gene correction of the mutation in the antibiotic resistance gene. Correction of the mutation results in the expression of a fusion protein that carries a marker ligand binding site and when the fusion protein binds the ligand, a green fluorescence is emitted. The ligand is produced by Aurora Biosciences and can readily diffuse into cells enabling a measurement of corrected protein function; the protein must bind the ligand directly to induce fluorescence. Hence cells bearing the corrected plasmid gene appear green while "uncorrected" cells remain colorless.

Figure 6. *Z-series imaging of corrected cells.* Serial cross-sections of the HeLa cell represented in Figure 5 are produced by Zeiss 510 LSM confocal microscope revealing that the fusion protein is contained within the cell.

Figure 7. *Hygromycin-eGFP target plasmids.* (A) Plasmid pAURHYG(ins)GFP contains a single base insertion mutation between nucleotides 136 and 137, at codon 46, of the Hygromycin B coding sequence (cds) which is transcribed from the constitutive ADH1 promoter. The target sequence presented below indicates the deletion of an A and the substitution of a C for a T directed by the oligonucleotides to re-establish the resistant phenotype. (B) Plasmid pAURHYG(rep)GFP contains a base substitution mutation introducing a G at nucleotide 137, at codon 46, of the Hygromycin B coding sequence (cds). The target sequence presented below the diagram indicates the amino acid conservative replacement of G with C, restoring gene function..

Figure 8. *Oligonucleotides for correction of hygromycin resistance gene.* The sequence of the oligonucleotides used in experiments to assay correction of a hygromycin resistance gene are shown. DNA residues are shown in capital letters, RNA residues are shown in lowercase and nucleotides with a phosphorothioate backbone are capitalized and underlined.

Figure 9. *pAURNeo(-)FlAsH plasmid.* This figure describes the plasmid structure, target sequence, oligonucleotides, and the basis for detection of the gene alteration event by fluorescence.

Figure 10. pYESHyg(x)eGFP plasmid. This plasmid is a construct similar to the pAURHyg(x)eGFP construct shown in Figure 7, except the promoter is the inducible GAL1 promoter. This promoter is inducible with galactose, leaky in the presence of raffinose, and repressed in the presence of dextrose.

The following examples are provided by way of illustration only, and are not intended to limit the scope of the invention disclosed herein.

EXAMPLE 1
Assay Method For Base Alteration
And Preferred Oligonucleotide Selection

In this example, single-stranded and double-hairpin oligonucleotides with chimeric backbones (see Figure 1 for structures (A and B) and sequences (C and D) of assay oligonucleotides) are used to correct a point mutation in the kanamycin gene of pK^{s}m4021 (Figure 2) or the tetracycline gene of pT$^{s}\Delta$208 (Figure 3). All kan oligonucleotides share the same 25 base sequence surrounding the target base identified for change, just as all tet oligonucleotides do. The sequence is given in Figures 1C and Figure 1D. Each plasmid contains a functional ampicillin gene. Kanamycin gene function is restored

when a G at position 4021 is converted to a C (via a substitution mutation); tetracycline gene function is restored when a deletion at position 208 is replaced by a C (via frameshift mutation). A separate plasmid, pAURNeo(-)FlAsH (Figure 9), bearing the kan^s gene is used in the cell culture experiments. This plasmid was constructed by inserting a synthetic expression cassette containing a neomycin phosphotransferase (kanamycin resistance) gene and an extended reading frame that encodes a receptor for the FlAsH ligand into the pAUR123 shuttle vector (Panvera Corp., Madison, WI). The resulting construct replicates in *S. cerevisiae* at low copy number, confers resistance to aureobasidinA and constitutively expresses either the Neo+/FlAsH fusion product (after alteration) or the truncated Neo-/FlAsH product (before alteration) from the ADH1 promoter. By extending the reading frame of this gene to code for a unique peptide sequence capable of binding a small ligand to form a fluorescent complex, restoration of expression by correction of the stop codon can be detected in real time using confocal microscopy. Additional constructs can be made to test additional gene alteration events.

We also construct three mammalian expression vectors, pHyg(rep)eGFP, pHyg(Δ)eGFP, pHyg(ins)eGFP, that contain a substitution mutation at nucleotide 137 of the hygromycin-B coding sequence. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. All point mutations create a nonsense termination codon at residue 46. We use pHygEGFP plasmid (Invitrogen, CA) DNA as a template to introduce the mutations into the hygromycin-eGFP fusion gene by a two step site-directed mutagenesis PCR protocol. First, we generate overlapping 5' and a 3' amplicons surrounding the mutation site by PCR for each of the point mutation sites. A 215 bp 5' amplicon for the (rep), (Δ) or (ins) was generated by polymerization from oligonucleotide primer HygEGFPf (5'-AATACGACTCACTATAGG-3') to primer Hygrepr (5'GACCTATCCACGCCCTCC-3'), HygΔr (5'-GACTATCCACGCCCTCC-3'), or Hyginsr (5'-GACATTATCCACGCCCTCC-3'), respectively. We generate a 300bp 3' amplicon for the (rep), (Δ) or (ins) by polymerization from oligonucleotide primers Hygrepf (5'-CTGGGATAGGTCCTGCGG-3'), HygΔf (5'-CGTGGATAGTCCTGCGG-3'), Hyginsf (5'-CGTGGATAATGTCCTGCGG-3'), respectively to primer HygEGFPr (5'-AAATCACGCCATGTAGTG-3'). We mix 20 ng of each of the resultant 5' and 3' overlapping amplicon mutation sets and use the mixture as a template to amplify a 523 bp fragment of the Hygromycin gene spanning the KpnI and RsrII restriction endonuclease sites. We use the Expand PCR system (Roche) to generate all amplicons with 25 cycles of denaturing at 94°C for 10 seconds, annealing at 55°C for 20 seconds and elongation at 68°C for 1 minute. We digest 10 μg of vector pHygEGFP and 5 μg of the resulting fragments for each mutation with KpnI and RsrII (NEB) and gel purify the fragment for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ration using T4

DNA ligase (Roche). We screen clones by restriction digest, confirm the mutation by Sanger dideoxy chain termination sequencing and purify the plasmid using a Qiagen maxiprep kit.

Oligonucleotide synthesis and cells. Chimeric oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) are synthesized using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, each oligonucleotide is gel-purified using, for example, procedures such as those described in Gamper *et al., Biochem.* 39, 5808-5816 (2000) and the concentrations determined spectrophotometrically (33 or 40 µg/ml per A_{260} unit of single-stranded or hairpin oligomer). HUH7 cells are grown in DMEM, 10% FBS, 2mM glutamine, 0.5% pen/strep. The *E.coli* strain, DH10B, is obtained from Life Technologies (Gaithersburg, MD); DH10B cells contain a mutation in the RECA gene (*recA*).

Cell-free extracts. We prepare cell-free extracts from HUH7 cells or other mammalian cells, as follows. We employ this protocol with essentially any mammalian cell including, for example, H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma). We harvest approximately $2x10^8$ cells. We then wash the cells immediately in cold hypotonic buffer (20 mM HEPES, pH7.5; 5 mM KCl; 1.5 mM $MgCl_2$; 1 mM DTT) with 250 mM sucrose. We then resuspend the cells in cold hypotonic buffer without sucrose and after 15 minutes we lyse the cells with 25 strokes of a Dounce homogenizer using a tight fitting pestle. We incubate the lysed cells for 60 minutes on ice and centrifuge the sample for 15 minutes at 12000x*g*. The cytoplasmic fraction is enriched with nuclear proteins due to the extended co-incubation of the fractions following cell breakage. We then immediately aliquote and freeze the supernatant at -80°C. We determine the protein concentration in the extract by the Bradford assay.

We also perform these experiments with cell-free extracts obtained from fungal cells, including, for example, *S. cerevisiae* (yeast), *Ustilago maydis*, and *Candida albicans*. For example, we grow yeast cells into log phase in 2L YPD medium for 3 days at 30°C. We then centrifuge the cultures at 5000x*g*, resuspend the pellets in a 10% sucrose, 50 mM Tris, 1mM EDTA lysis solution and freeze them on dry ice. After thawing, we add KCl, spermidine and lyticase to final concentrations of 0.25 mM, 5 mM and 0.1 mg/ml, respectively. We incubate the suspension on ice for 60 minutes, add PMSF and Triton X100 to final concentrations of 0.1 mM and 0.1% and continue to incubate on ice for 20 minutes. We centrifuge the lysate at 3000x*g* for 10 minutes to remove larger debris. We then remove the supernatant and clarify it by centrifuging at 30000x*g* for 15 minutes. We then add glycerol to the clarified extract to a

concentration of 10% (v/v) and freeze aliquots at -80°C. We determine the protein concentration of the extract by the Bradford assay.

Reaction mixtures of 50 µl are used, consisting of 10-30 µg protein of cell-free extract, which can be optionally substituted with purified proteins or enriched fractions, about 1.5 µg chimeric double-hairpin oligonucleotide or 0.55 µg single-stranded molecule (3S/25G or 6S/25G, see Figure 1), and 1 µg of plasmid DNA (see Figures 2 and 3) in a reaction buffer of 20 mM Tris, pH 7.4, 15 mM $MgCl_2$, 0.4 mM DTT, and 1.0 mM ATP. Reactions are initiated with extract and incubated at 30°C for 45 min. The reaction is stopped by placing the tubes on ice and then immediately deproteinized by two phenol/chloroform (1:1) extractions. Samples are then ethanol precipitated. The nucleic acid is pelleted at 15,000 r.p.m. at 4°C for 30 min., is washed with 70% ethanol, resuspended in 50 µl H_20, and is stored at -20°C. 5 µl of plasmid from the resuspension (~100 ng) was transfected in 20 µl of DH10B cells by electroporation (400 V, 300 µF, 4 kΩ) in a Cell-Porator apparatus (Life Technologies). After electroporation, cells are transferred to a 14 ml Falcon snap-cap tube with 2 ml SOC and shaken at 37°C for 1 h. Enhancement of final kan colony counts is achieved by then adding 3 ml SOC with 10 µg/ml kanamycin and the cell suspension is shaken for a further 2 h at 37°C. Cells are then spun down at 3750 x g and the pellet is resuspended in 500 µl SOC. 200 µl is added undiluted to each of two kanamycin (50 µg/ml) agar plates and 200 µl of a 10^5 dilution is added to an ampicillin (100 µg/ml) plate. After overnight 37°C incubation, bacterial colonies are counted using an Accucount 1000 (Biologics). Gene conversion effectiveness is measured as the ratio of the average of the kan colonies on both plates per amp colonies multiplied by 10^{-5} to correct for the amp dilution.

The following procedure can also be used. 5 µl of resuspended reaction mixtures (total volume 50 µl) are used to transform 20 µl aliquots of electro-competent ΔH10B bacteria using a Cell-Porator apparatus (Life Technologies). The mixtures are allowed to recover in 1 ml SOC at 37°C for 1 hour at which time 50 µg/ml kanamycin or 12 µg/ml tetracycline is added for an additional 3 hours. Prior to plating, the bacteria are pelleted and resuspended in 200 µ1 of SOC. 100 µl aliquots are plated onto kan or tet agar plates and 100 µl of a 10^{-4} dilution of the cultures are concurrently plated on agar plates containing 100 µg/ml of ampicillin. Plating is performed in triplicate using sterile Pyrex beads. Colony counts are determined by an Accu-count 1000 plate reader (Biologics). Each plate contains 200-500 ampicillin resistant colonies or 0-500 tetracycline or kanamycin resistant colonies. Resistant colonies are selected for plasmid extraction and DNA sequencing using an ABI Prism kit on an ABI 310 capillary sequencer (PE Biosystems).

Chimeric single-stranded oligonucleotides. In Figure 1 the upper strands of chimeric oligonucleotides I and II are separated into pathways resulting in the generation of single-stranded oligonucleotides that contain (Figure 1A) 2'-O-methyl RNA nucleotides or (Figure 1B) phosphorothioate linkages. Fold changes in repair activity for correction of kan^s in the HUH7 cell-free extract are presented in parenthesis. Each single-stranded oligonucleotide is 25 bases in length and contains a G residue mismatched to the complementary sequence of the kan^s gene.

Molecules bearing 3, 6, 8, 10 and 12 phosphorothioate linkages in the terminal regions at each end of a backbone with a total of 24 linkages (25 bases) are tested in the kan^s system. Alternatively, molecules bearing 2, 4, 5, 7, 9 and 11 in the terminal regions at each end are tested. The results of one such experiment, presented in Table 1 and Figure 1B, illustrate an enhancement of correction activity directed by some of these modified structures. In this illustrative example, the most efficient molecules contained 3 or 6 phosphorothioate linkages at each end of the 25-mer; the activities are approximately equal (molecules IX and X with results of 3.09 and 3.7 respectively). A reduction in alteration activity may be observed as the number of modified linkages in the molecule is further increased. Interestingly, a single-strand molecule containing 24 phosphorothioate linkages is minimally active suggesting that this backbone modification when used throughout the molecule supports only a low level of targeted gene repair or alteration. Such a non-altering, completely modified molecule can provide a baseline control for determining efficiency of correction for a specific oligonucleotide molecule of known sequence in defining the optimum oligonucleotide for a particular alteration event.

The efficiency of gene repair directed by phosphorothioate-modified, single-stranded molecules, in a length dependent fashion, led us to examine the length of the RNA modification used in the original chimera as it relates to correction. Construct III represents the "RNA-containing" strand of chimera I and, as shown in Table 1 and Figure 2A, it promotes inefficient gene repair. But, as shown in the same figure, reducing the RNA residues on each end from 10 to 3 increases the frequency of repair. At equal levels of modification, however, 25-mers with 2'-O-methyl ribonucleotides were less effective gene repair agents than the same oligomers with phosphorothioate linkages. These results reinforce the fact that an RNA containing oligonucleotide is not as effective in promoting gene repair or alteration as a modified DNA oligonucleotide.

Repair of the kanamycin mutation requires a G→C exchange. To confirm that the specific desired correction alteration was obtained, colonies selected at random from multiple experiments are processed and the isolated plasmid DNA is sequenced. As seen in Figure 4, colonies generated through the action of the single-stranded molecules 3S/25G (IX), 6S/25G (X) and 8S/25G (XI) respectively

contained plasmid molecules harboring the targeted base correction. While a few colonies appeared on plates derived from reaction mixtures containing 25-mers with 10 or 12 thioate linkages on both ends, the sequences of the plasmid molecules from these colonies contain nonspecific base changes. In these illustrative examples, the second base of the codon is changed (see Figure 3). These results show that modified single-strands can direct gene repair, but that efficiency and specificity are reduced when the 25-mers contain 10 or more phosphorothioate linkages at each end.

In Figure 1, the numbers 3, 6, 8, 10, 12 and 12.5 respectively indicate how many phosphorothioate linkages (S) or 2'-O-methyl RNA nucleotides (R) are at each end of the examplified molecule although other molecules with 2, 4, 5, 7, 9 and 11 modifications at each end can also be tested. Hence oligo 12S/25G represents a 25-mer oligonucleotide which contains 12 phosphorothioate linkages on each side of the central G target mismatch base producing a fully phosphorothioate linked backbone, displayed as a dotted line. The dots are merely representative of a linkage in the figure and do not depict the actual number of linkages of the oligonucleotide. Smooth lines indicate DNA residues, wavy lines indicate 2'-O-methyl RNA residues and the carat indicates the mismatched base site (G).

Correction of a mutant kanamycin gene in cultured mammalian cells. The experiments are performed using different mammalian cells, including, for example, 293 cells (transformed human primary kidney cells), HeLa cells (human cervical carcinoma), and H1299 (human epithelial carcinoma, non-small cell lung cancer). HeLa cells are grown at 37°C and 5% CO_2 in a humidified incubator to a density of 2 x 10^5 cells/ml in an 8 chamber slide (Lab-Tek). After replacing the regular DMEM with Optimem, the cells are co-transfected with 10 μg of plasmid pAURNeo(-)FlAsH and 5 μg of modified single-stranded oligonucleotide (3S/25G) that is previously complexed with 10 μg lipofectamine, according to the manufacturer's directions (Life Technologies). The cells are treated with the liposome-DNA-oligo mix for 6 hrs at 37°C. Treated cells are washed with PBS and fresh DMEM is added. After a 16-18 hr recovery period, the culture is assayed for gene repair. The same oligonucleotide used in the cell-free extract experiments is used to target transfected plasmid bearing the kan^s gene. Correction of the point mutation in this gene eliminates a stop codon and restores full expression. This expression can be detected by adding a small non-fluorescent ligand that bound to a C-C-R-E-C-C sequence in the genetically modified carboxy terminus of the kan protein, to produce a highly fluorescent complex (FlAsH system, Aurora Biosciences Corporation). Following a 60 min incubation at room temperature with the ligand (FlAsH-EDT2), cells expressing full length kan product acquire an intense green fluorescence detectable by fluorescence microscopy using a fluorescein filter set. Similar experiments are performed using the HygeGFP target as described in Example 2 with a variety of mammalian cells, including, for

example, COS-1 and COS-7 cells (African green monkey), and CHO-K1 cells (Chinese hamster ovary). The experiments are also performed with PG12 cells (rat pheochromocytoma) and ES cells (human embryonic stem cells).

Summary of experimental results. Tables 1, 2 and 3 respectively provide data on the efficiency of gene repair directed by single-stranded oligonucleotides. Table 1 presents data using a cell-free extract from human liver cells (HUH7) to catalyze repair of the point mutation in plasmid pkan^{s}m4021 (see Figure 1). Table 2 illustrates that the oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity. Table 3 illustrates data from the repair of a frameshift mutation (Figure 3) in the tet gene contained in plasmid pTetΔ208. Table 4 illustrates data from repair of the pkan^{s}m4021 point mutation catalyzed by plant cell extracts prepared from canola and musa (banana). Colony numbers are presented as kan^r or tet^r and fold increases (single strand versus double hairpin) are presented for kan^r in Table 1.

Figure 5A is a confocal picture of HeLa cells expressing the corrected fusion protein from an episomal target. Gene repair is accomplished by the action of a modified single-stranded oligonucleotide containing 3 phosphorothioate linkages at each end (3S/25G). Figure 5B represents a "Z-series" of HeLa cells bearing the corrected fusion gene. This series sections the cells from bottom to top and illustrates that the fluorescent signal is "inside the cells".

Results. In summary, we have designed a novel class of single-stranded oligonucleotides with backbone modifications at the termini and demonstrate gene repair/conversion activity in mammalian and plant cell-free extracts. We confirm that the all DNA strand of the RNA-DNA double-stranded double hairpin chimera is the active component in the process of gene repair. In some cases, the relative frequency of repair by the novel oligonucleotides of the invention is elevated approximately 3-4-fold when compared to frequencies directed by chimeric RNA-DNA double hairpin oligonucleotides.

This strategy centers around the use of extracts from various sources to correct a mutation in a plasmid using a modified single-stranded or a chimeric RNA-DNA double hairpin oligonucleotide. A mutation is placed inside the coding region of a gene conferring antibiotic resistance in bacteria, here kanamycin or tetracycline. The appearance of resistance is measured by genetic readout in *E.coli* grown in the presence of the specified antibiotic. The importance of this system is that both phenotypic alteration and genetic inheritance can be measured. Plasmid pK^{s}m4021 contains a mutation (T$\rightarrow$G) at residue 4021 rendering it unable to confer antibiotic resistance in *E.coli.* This point mutation is targeted for repair by oligonucleotides designed to restore kanamycin resistance. To avoid concerns of

plasmid contamination skewing the colony counts, the directed correction is from G→C rather than G→T (wild-type). After isolation, the plasmid is electroporated into the DH10B strain of *E.coli*, which contains inactive RecA protein. The number of kanamycin colonies is counted and normalized by ascertaining the number of ampicillin colonies, a process that controls for the influence of electroporation. The number of colonies generated from three to five independent reactions was averaged and is presented for each experiment. A fold increase number is recorded to aid in comparison.

The original RNA-DNA double hairpin chimera design, e.g., as disclosed in U.S. Patent 5,565,350, consists of two hybridized regions of a single-stranded oligonucleotide folded into a double hairpin configuration. The double-stranded targeting region is made up of a 5 base pair DNA/DNA segment bracketed by 10 base pair RNA/DNA segments. The central base pair is mismatched to the corresponding base pair in the target gene. When a molecule of this design is used to correct the kan^s mutation, gene repair is observed (I in Figure 1A). Chimera II (Figure 1B) differs partly from chimera I in that only the DNA strand of the double hairpin is mismatched to the target sequence. When this chimera was used to correct the kan^s mutation, it was twice as active. In the same study, repair function could be further increased by making the targeting region of the chimera a continuous RNA/DNA hybrid.

Frame shift mutations are repaired. By using plasmid pT$^s\Delta$208, described in Figure 1(C) and Figure 3, the capacity of the modified single-stranded molecules that showed activity in correcting a point mutation, can be tested for repair of a frameshift. To determine efficiency of correction of the mutation, a chimeric oligonucleotide (Tet I), which is designed to insert a T residue at position 208, is used. A modified single-stranded oligonucleotide (Tet IX) directs the insertion of a T residue at this same site. Figure 3 illustrates the plasmid and target bases designated for change in the experiments. When all reaction components are present (extract, plasmid, oligomer), tetracycline resistant colonies appear. The colony count increases with the amount of oligonucleotide used up to a point beyond which the count falls off (Table 3). No colonies above background are observed in the absence of either extract or oligonucleotide, nor when a modified single-stranded molecule bearing perfect complementarity is used. Figure 3 represents the sequence surrounding the target site and shows that a T residue is inserted at the correct site. We have isolated plasmids from fifteen colonies obtained in three independent experiments and each analyzed sequence revealed the same precise nucleotide insertion. These data suggest that the single-stranded molecules used initially for point mutation correction can also repair nucleotide deletions.

Comparison of phosphorothioate oligonucleotides to 2'-O-methyl substituted oligonucleotides. From a comparison of molecules VII and XI, it is apparent that gene repair is more

subject to inhibition by RNA residues than by phosphorothioate linkages. Thus, even though both of these oligonucleotides contain an equal number of modifications to impart nuclease resistance, XI (with 16 phosphorothioate linkages) has good gene repair activity while VII (with 16 2'-O-methyl RNA residues) is inactive. Hence, the original chimeric double hairpin oligonucleotide enabled correction directed, in large part, by the strand containing a large region of contiguous DNA residues.

Oligonucleotides can target multiple nucleotide alterations within the same template. The ability of individual single-stranded oligonucleotides to correct multiple mutations in a single target template is tested using the plasmid pK^{s}m4021 and the following single-stranded oligonucleotides modified with 3 phosphorothioate linkages at each end (indicated as underlined nucleotides): Oligo1 is a 25-mer with the sequence TTCGATAAGCCTAT**G**CTGACCCGTG corrects the original mutation present in the kanamycin resistance gene of pK^{s}m4021 as well as directing another alteration 2 basepairs away in the target sequence (both indicated in boldface); Oligo2 is a 70-mer with the 5'-end sequence TTCGGCTACGACTGGGCACAACAGACAA**T**TGGC with the remaining nucleotides being completely complementary to the kanamycin resistance gene and also ending in 3 phosphorothioate linkages at the 3' end. Oligo2 directs correction of the mutation in pK^{s}m4021 as well as directing another alteration 21 basepairs away in the target sequence (both indicated in boldface).

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pK^{s}M4021 plasmid. These include, for example, a second 25-mer that alters two nucleotides that are three nucleotides apart with the sequence 5'-TTGTGCCCAGTC**G**TA**T**CCGAATAGC-3'; a 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-CATCAGAGCAGCC**A**ATTGTCTGTTGTGCCCAGTC**G**TAGCCGAA TAGCCTCTCCACCCAAGCGGCCGGAGA-3'; and another 70-mer that alters two nucleotides that are 21 nucleotides apart with the sequence 5'-GCTGACAGCCGGAACACGGCGGCATCAGAGCAGCC**A**ATTGTCTGTTGTGCCCAGTC**G**TAGCCGAAT AGCCT-3'. The nucleotides in the oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same way as the other oligonucleotides of the invention.

We assay correction of the original mutation in pK^{s}m4021 by monitoring kanamycin resistance (the second alterations which are directed by Oligo2 and Oligo3 are silent with respect to the kanamycin resistance phenotype). In addition, in experiments with Oligo2, we also monitor cleavage of the resulting plasmids using the restriction enzyme Tsp509I which cuts at a specific site present only when the second alteration has occurred (at ATT in Oligo2). We then sequence these clones to

determine whether the additional, silent alteration has also been introduced. The results of an analysis are presented below:

	Oligo1 (25-mer)	Oligo2 (70-mer)
Clones with both sites changed	9	7
Clones with a single site changed	0	2
Clones that were not changed	4	1

Nuclease sensitivity of unmodified DNA oligonucleotide. Electrophoretic analysis of nucleic acid recovered from the cell-free extract reactions conducted here confirm that the unmodified single-stranded 25-mer did not survive incubation whereas greater than 90% of the terminally modified oligos did survive (as judged by photo-image analyses of agarose gels).

Plant extracts direct repair. The modified single-stranded constructs can be tested in plant cell extracts. We have observed gene alteration using extracts from multiple plant sources, including, for example, Arabidopsis, tobacco, banana, maize, soybean, canola, wheat, spinach as well as spinach chloroplast extract. We prepare the extracts by grinding plant tissue or cultured cells under liquid nitrogen with a mortar and pestle. We extract 3 ml of the ground plant tissue with 1.5 ml of extraction buffer (20 mM HEPES, pH7.5; 5 mM Kcl; 1.5 mM $MgCl_2$; 10 mM DTT; 10% [v/v] glycerol; and 1 % [w/v] PVP). We then homogenize the samples with 15 strokes of a Dounce homogenizer. Following homogenization, we incubate the samples on ice for 1 hour and centrifuge at 3000x*g* for 5 minutes to remove plant cell debris. We then determine the protein concentration in the supernatants (extracts) by Bradford assay. We dispense 100 µg (protein) aliquots of the extracts which we freeze in a dry ice-ethanol bath and store at -80°C.

We describe experiments using two sources here: a dicot (canola) and a monocot (banana, *Musa acuminata* cv. Rasthali). Each vector directs gene repair of the kanamycin mutation (Table 4); however, the level of correction is elevated 2-3 fold relative to the frequency observed with the chimeric oligonucleotide. These results are similar to those observed in the mammalian system wherein a significant improvement in gene repair occurred when modified single-stranded molecules were used.

Tables are attached hereto.

Table I

Gene repair activity is directed by single-stranded oligonucleotides.

Oligonucleotide	Plasmid	Extract (ug)	kan^r colonies	Fold increase
I	pK^{S}m4021	10	300	
I	↓	20	418	1.0x
II		10	537	
II		20	748	1.78x
III		10	3	
III		20	5	0.01x
IV		10	112	
IV		20	96	0.22x
V		10	217	
V		20	342	0.81x
VI		10	6	
VI		20	39	0.093x
VII		10	0	
VII		20	0	0x
VIII		10	3	
VIII		20	5	0.01x
IX		10	936	
IX		20	1295	3.09x
X		10	1140	
X		20	1588	3.7x
XI		10	480	
XI		20	681	1.6x
XII		10	18	
XII		20	25	0.059x
XIII		10	0	
XIII		20	4	0.009x
-		20	0	
I		-	0	

Plasmid pK^{s}m4021 (1μg), the indicated oligonucleotide (1.5 μg chimeric oligonucleotide or 0.55 μg single-stranded oligonucleotide; molar ratio of oligo to plasmid of 360 to 1) and either 10 or 20 μg of HUH7 cell-free extract were incubated 45 min at 37°C. Isolated plasmid DNA was electroporated into *E. coli* (strain DH10B) and the number of kan^r colonies counted. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of three

experiments (standard deviation usually less than +/- 15%). Fold increase is defined relative to 418 kan^r colonies (second reaction) and in all reactions was calculated using the 20μg sample.

Table II

Modified single-stranded oligomers are not dependent on MSH2 or MSH3 for optimal gene repair activity.

A.

Oligonucleotide	Plasmid	Extract	kan^r colonies
IX (3S/25G)	↓	HUH7	637
X (6S/25G)	↓	HUH7	836
IX	↓	$MEF2^{-/-}$	781
X	↓	$MEF2^{-/-}$	676
IX	↓	$MEF3^{-/-}$	582
X	↓	$MEF3^{-/-}$	530
IX	↓	$MEF^{+/+}$	332
X	↓	$MEF^{+/+}$	497
-	↓	$MEF2^{-/-}$	10
-	↓	$MEF3^{-/-}$	5
-	↓	$MEF^{+/+}$	14

Chimeric oligonucleotide (1.5 μg) or modified single-stranded oligonucleotide (0.55 μg) was incubated with 1μg of plasmid pK^sm4021 and 20μg of the indicated extracts. MEF represents mouse embryonic fibroblasts with either MSH2 ($2^{-/-}$) or MSH3 ($3^{-/-}$) deleted. $MEF^{+/+}$ indicates wild-type mouse embryonic fibroblasts. The other reaction components were then added and processed through the bacterial readout system. The data represent the number of kanamycin resistant colonies per 10^6 ampicillin resistant colonies.

Table III

Frameshift mutation repair is directed by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	tet^r colonies
Tet IX (3S/25A; 0.5 µg)	pT^{s}Δ208 (1µg)	-	0
-		20µg	0
Tet IX (0.5 µg)			48
Tet IX (1.5 µg)			130
Tet IX (2.0 µg)			68
Tet I (chimera; 1.5 µg)			48

Each reaction mixture contained the indicated amounts of plasmid and oligonucleotide. The extract used for these experiments came from HUH7 cells. The data represent the number of tetracycline resistant colonies per 10^6 ampicillin resistant colonies generated from the same reaction and is the average of 3 independent experiments. Tet I is a chimeric oligonucleotide and Tet IX is a modified single-stranded oligonucleotide that are designed to insert a T residue at position 208 of pT^{s}Δ208. These oligonucleotides are equivalent to structures I and IX in Figure 2.

Table IV

Plant cell-free extracts support gene repair by single-stranded oligonucleotides

Oligonucleotide	Plasmid	Extract	kan^r colonies
II (chimera)	pK^Sm4021	30μg Canola	337
IX (3S/25G)		Canola	763
X (6S/25G)		Canola	882
II		*Musa*	203
IX		*Musa*	343
X		*Musa*	746
-		Canola	0
-		*Musa*	0
IX		- Canola	0
X		- *Musa*	0

Canola or Musa cell-free extracts were tested for gene repair activity on the kanamycin-sensitive gene as previously described in (18). Chimeric oligonucleotide II (1.5 μg) and modified single-stranded oligonucleotides IX and X (0.55μg) were used to correct pK^Sm4021. Total number of kan^r colonies are present per 10^7 ampicillin resistant colonies and represent an average of four independent experiments.

Table V

Gene repair activity in cell-free extracts prepared from yeast (Saccharomyces cerevisiae)

Cell-type	Plasmid	Chimeric Oligo	SS Oligo	$kan^r/amp^r \times 10^6$
Wild type	pKan^{s}m4021	1μg		0.36
Wild type			1μg	0.81
ΔRAD52		1μg		10.72
ΔRAD52			1μg	17.41
ΔPMS1		1μg		2.02
ΔPMS1			1μg	3.23

In this experiment, the kan^s gene in pKan^{s}4021 is corrected by either a chimeric double-hairpin oligonucleotide or a single-stranded oligonucleotide containing three thioate linkages at each end (3S/25G).

EXAMPLE 2
Yeast Cell Targeting Assay Method for Base Alteration and Preferred Oligonucleotide Selection

In this example, single-stranded oligonucleotides with modified backbones and double-hairpin oligonucleotides with chimeric, RNA-DNA backbones are used to measure gene repair using two episomal targets with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair. These plasmids are pAURHYG(rep)GFP, which contains a point mutation in the hygromycin resistance gene (Figure 7), pAURHYG(ins)GFP, which contains a single-base insertion in the hygromycin resistance gene (Figure 7) and pAURHYG(Δ)GFP which has a single base deletion. We also use the plasmid containing a wild-type copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)GFP, as a control. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, at codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)GFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, at codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene.

We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows. (rep) indicates a T137→G replacement, (Δ) represents a deletion of the G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)EGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μg pAUR123 vector DNA, as well as, 10 μg of each pHyg(x)EGFP construct with KpnI and SalI (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pHygEGFP vector at 3:1 molar ration using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify using a Qiagen maxiprep kit.

We use this system to assay the ability of five oligonucleotides (shown in Figure 8) to support correction under a variety of conditions. The oligonucleotides which direct correction of the mutation in pAURHYG(rep)GFP can also direct correction of the mutation in pAURHYG(ins)GFP. Three of the four oligonucleotides (HygE3T/25, HygE3T/74 and HygGG/Rev) share the same 25-base sequence surrounding the base targeted for alteration. HygGG/Rev is an RNA-DNA chimeric double hairpin

oligonucleotide of the type described in the prior art. One of these oligonucleotides, HygE3T/74, is a 74-base oligonucleotide with the 25-base sequence centrally positioned. The fourth oligonucleotide, designated HygE3T/74α, is the reverse complement of HygE3T/74. The fifth oligonucleotide, designated Kan70T, is a non-specific, control oligonucleotide which is not complementary to the target sequence. Alternatively, an oligonucleotide of identical sequence but lacking a mismatch to the target or a completely thioate modified oligonucleotide or a completely 2-0-methylated modified oligonucleotide may be used as a control.

Oligonucleotide synthesis and cells. We synthesized and purified the chimeric, double-hairpin oligonucleotides and single-stranded oligonucleotides (including those with the indicated modifications) as described in Example 1. Plasmids used for assay were maintained stably in yeast (*Saccharomyces cerevisiae*) strain LSY678 *MATα* at low copy number under aureobasidin selection. Plasmids and oligonucleotides are introduced into yeast cells by electroporation as follows: to prepare electrocompetent yeast cells, we inoculate 10 ml of YPD media from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We then add 30 ml of fresh YPD media to the overnight cultures and continue shaking at 30°C until the OD_{600} was between 0.5 and 1.0 (3-5 hours). We then wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We then centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 µl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 µl of cells with 5 µg of nucleic acid, unless otherwise stated, and incubate on ice for 5 minutes. We then transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 µF, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 1 ml YPD supplemented with 1M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We then spread 200 µl of this culture on selective plates containing 300 µg/ml hygromycin and spread 200 µl of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We then count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies.

Frameshift mutations are repaired in yeast cells. We test the ability of the oligonucleotides shown in Figure 8 to correct a frameshift mutation *in vivo* using LSY678 yeast cells containing the plasmid pAURHYG(ins)GFP. These experiments, presented in Table 6, indicate that these oligonucleotides can support gene correction in yeast cells. These data reinforce the results described in

Example 1 indicating that oligonucleotides comprising phosphorothioate linkages facilitate gene correction much more efficiently than control duplex, chimeric RNA-DNA oligonucleotides. This gene correction activity is also specific as transformation of cells with the control oligonucleotide Kan70T produced no hygromycin resistant colonies above background and thus Kan70T did not support gene correction in this system. In addition, we observe that the 74-base oligonucleotide (HygE3T/74) corrects the mutation in pAURHYG(ins)GFP approximately five-fold more efficiently than the 25-base oligonucleotide (HygE3T/25). We also perform control experiments with LSY678 yeast cells containing the plasmid pAURHYG(wt)GFP. With this strain we observed that even without added oligonucleotides, there are too many hygromycin resistant colonies to count.

We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in the pAURHYG(x)eGFP plasmid. These include, for example, one that alters two basepairs that are 3 nucleotides apart is a 74-mer with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGG**G**TA**C**GTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTAC-3'; a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAA**C**AGCTGCGCCGATGGTTTCTAC-3'; and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATA**C**GTCCTGCGGGTAAATAGCTGCGCCGA**C**GGTTTCTAC. The nucleotides in these oligonucleotides that direct alteration of the target sequence are underlined and in boldface. These oligonucleotides are modified in the same ways as the other oligonucleotides of the invention.

Oligonucleotides targeting the sense strand direct gene correction more efficiently. We compare the ability of single-stranded oligonucleotides to target each of the two strands of the target sequence of both pAURHYG(ins)GFP and pAURHYG(rep)GFP. These experiments, presented in Tables 7 and 8, indicate that an oligonucleotide, HygE3T/74α, with sequence complementary to the sense strand (i.e. the strand of the target sequence that is identical to the mRNA) of the target sequence facilitates gene correction approximately ten-fold more efficiently than an oligonucleotide, HygE3T/74, with sequence complementary to the non-transcribed strand which serves as the template for the synthesis of RNA. As indicated in Table 7, this effect was observed over a range of oligonucleotide concentrations from 0-3.6 μg, although we did observe some variability in the difference between the two oligonucleotides (indicated in Table 7 as a fold difference between HygE3T/74α and HygE3T/74). Furthermore, as shown in Table 8, we observe increased efficiency of correction by HygE3T/74α relative to HygE3T/74 regardless of whether the oligonucleotides were used to correct the base substitution

mutation in pAURHYG(rep)GFP or the insertion mutation in pAURHYG(ins)GFP. The data presented in Table 8 further indicate that the single-stranded oligonucleotides correct a base substitution mutation more efficiently than an insertion mutation. However, this last effect was much less pronounced and the oligonucleotides of the invention are clearly able efficiently to correct both types of mutations in yeast cells. In addition, the role of transcription is investigated using plasmids with inducible promoters such as that described in Figure 10.

Optimization of oligonucleotide concentration. To determine the optimal concentration of oligonucleotide for the purpose of gene alteration, we test the ability of increasing concentrations of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678. We chose this assay system because our previous experiments indicated that it supports the highest level of correction. However, this same approach could be used to determine the optimal concentration of any given oligonucleotide. We test the ability of Hyg3T/74α to correct the mutation in pAURHYG(rep)GFP contained in yeast LSY678 over a range of oligonucleotide concentrations from 0-10.0 μg. As shown in Table 9, we observe that the correction efficiency initially increases with increasing oligonucleotide concentration, but then declines at the highest concentration tested.

Tables are attached hereto.

Table 6

Correction of an insertion mutation in pAURHYG(ins)GFP by HygGG/Rev, HygE3T/25 and HygE3T/74

Oligonucleotide Tested	Colonies on Hygromycin	Colonies on Aureobasidin (/10^5)	Correction Efficiency
HygGG/Rev	3	157	0.02
HygE3T/25	64	147	0.44
HygE3T/74	280	174	1.61
Kan70T	0	—	—

Table 7

An oligonucleotide targeting the sense strand of the target sequence corrects more efficiently.

Amount of Oligonucleotide (μg)	Colonies per hygromycin plate	
	HygE3T/74	HygE3T/74α
0	0	0
0.6	24	128 (8.4x)*
1.2	69	140 (7.5x)*
2.4	62	167 (3.8x)*
3.6	29	367 (15x)*

* The numbers in parentheses represent the fold increase in efficiency for targeting the non-transcribed strand as compared to the other strand of a DNA duplex that encodes a protein.

Table 8

Correction of a base substitution mutation is more efficient than correction of a frame shift mutation.

Oligonucleotide Tested (5 μg)	Plasmid tested (contained in LSY678)	
	pAURHYG(ins)GFP	pAURHYG(rep)GFP
HygE3T/74	72	277
HygE3T/74α	1464	2248
Kan70T	0	0

Table 9

Optimization of oligonucleotide concentration in electroporated yeast cells.

Amount (μg)	Colonies on hygromycin	Colonies on aureobasidin (/10^5)	Correction efficiency
0	0	67	0
1.0	5	64	0.08
2.5	47	30	1.57
5.0	199	33	6.08
7.5	383	39	9.79
10.0	191	33	5.79

Example 3
Cultured Cell Manipulation

Mononuclear cells are isolated from human umbilical cord blood of normal donors using Ficoll Hypaque (Pharmacia Biotech, Uppsala, Sweden) density centrifugation. CD34+ cells are immunomagnetically purified from mononuclear cells using either the progenitor or Multisort Kits (Miltenyi Biotec, Auburn, CA). Lin^-CD38^- cells are purified from the mononuclear cells using negative selection with StemSep system according to the manufacturer's protocol (Stem Cell Technologies, Vancouver, CA).

Cells used for microinjection are either freshly isolated or cryopreserved and cultured in Stem Medium (S Medium) for 2 to 5 days prior to microinjection. S Medium contains Iscoves' Modified Dulbecco's Medium without phenol red (IMDM) with 100 μg/ml glutamine/penicillin/streptomycin, 50 mg/ml bovine serum albumin, 50 μg/ml bovine pancreatic insulin, 1 mg/ml human transferrin, and IMDM; Stem Cell Technologies), 40 μg/ml low-density lipoprotein (LDL; Sigma, St. Louis, MO), 50 mM HEPEs buffer and 50 μM 2-mercaptoethanol, 20 ng/ml each of thrombopoietin, flt-3 ligand, stem cell factor and human IL-6 (Pepro Tech Inc., Rocky Hill, NJ). After microinjection, cells are detached and transferred in bulk into wells of 48 well plates for culturing.

35 mm dishes are coated overnight at 4° C with 50 μg/ml Fibronectin (FN) fragment CH-296 (Retronectin; TaKaRa Biomedicals, Panvera, Madison, WI) in phosphate buffered saline and washed with IMDM containing glutamine/penicillin/streptomycin. 300 to 2000 cells are added to cloning rings and attached to the plates for 45 minutes at 37° C prior to microinjection. After incubation, cloning rings are removed and 2 ml of S Medium are added to each dish for microinjection. Pulled injection needles with a range of 0.22 μ to 0.3 μ outer tip diameter are used. Cells are visualized with a microscope equipped with a temperature controlled stage set at 37° C and injected using an electronically interfaced Eppendorf Micromanipulator and Transjector. Successfully injected cells are intact, alive and remain attached to the plate post injection. Molecules that are flourescently labeled allow determination of the amount of oligonucleotide delivered to the cells.

For in vitro erythropoiesis from Lin^-CD38^- cells, the procedure of Malik, 1998 can be used. Cells are cultured in ME Medium for 4 days and then cultured in E Medium for 3 weeks. Erythropoiesis is evident by glycophorin A expression as well as the presence of red color representing the presence of hemoglobin in the cultured cells. The injected cells are able to retain their proliferative capacity and the ability to generate myeloid and erythoid progeny. CD34+ cells can convert a normal A (β^A) to sickle T (β^S) mutation in the β-globin gene or can be altered using any of the oligonucleotides of the invention herein for correction or alteration of a normal gene to a mutant gene. Alternatively, stem cells can be isolated from blood of humans having genetic disease mutations and the oligonucleotides of the invention can be used to correct a defect or to modify genomes within those cells.

Alternatively, non-stem cell populations of cultured cells can be manipulated using any method known to those of skill in the art including, for example, the use of polycations, cationic lipids, liposomes, polyethylenimine (PEI), electroporation, biolistics, calcium phophate precipitation, or any other method known in the art.

Notes on the tables presented below:

Each of the following tables presents, for the specified human gene, a plurality of mutations that are known to confer a clinically-relevant phenotype and, for each mutation, the oligonucleotides that can be used to correct the respective mutation site-specifically in the human genome according to the present invention.

The left-most column identifies each mutation and the clinical phenotype that the mutation confers.

For most entries, the mutation is identified at both the nucleic acid and protein level. At the amino acid level, mutations are presented according to the following standard nomenclature. The centered number identifies the position of the mutated codon in the protein sequence; to the left of the number is the wild type residue and to the right of the number is the mutant codon. Codon numbering is according to the Human Gene Mutation Database, Cardiff, Wales, UK (http://archive.uwcm.ac.uk/search/mg/allgenes). Terminator codons are shown as "TERM". At the nucleic acid level, the entire triplet of the wild type and mutated codons is shown.

The middle column presents, for each mutation, four oligonucleotides capable of repairing the mutation site-specifically in the human genome or in cloned human DNA including human DNA in artificial chromosomes, episomes, plasmids, or other types of vectors. The oligonucleotides of the invention, however, may include any of the oligonucleotides sharing portions of the sequence of the 121 base sequence. Thus, oligonucleotides of the invention for each of the depicted targets may be 18, 19, 20 up to about 121 nucleotides in length. Sequence may be added non-symmetrically.

All oligonucleotides are presented, per convention, in the 5' to 3' orientation. The nucleotide that effects the change in the genome is underlined and presented in bold.

The first of the four oligonucleotides for each mutation is a 121 nt oligonucleotide centered about the repair nucleotide. The second oligonucleotide, its reverse complement, targets the opposite strand of the DNA duplex for repair. The third oligonucleotide is the minimal 17 nt domain of the first oligonucleotide, also centered about the repair nucleotide. The fourth oligonucleotide is the reverse complement of the third, and thus represents the minimal 17 nt domain of the second.

The third column of each table presents the SEQ ID NO: of the respective repair oligonucleotide.

EXAMPLE 4

Adenosine Deaminase (ADA)

Adenosine deaminase (ADA, EC 3.5.4.4) catalyses the deamination of adenosine and 2'-deoxyadenosine to inosine or 2'-deoxyinosine respectively. ADA deficiency has been identified as the metabolic basis for 20-30% of cases with recessively inherited severe combined immunodeficiency (SCID). Affected infants are subject to recurrent chronic viral, fungal, protozoal, and bacterial infections and frequently present with persistent diarrhea, failure to thrive and candidiasis. In patients homozygous for ADA deficiency, 2'-deoxyadenosine accumulating during the rapid turnover of cells rich in DNA is converted back to dATP, either by adenosine kinase or deoxycytidine kinase. Many hypotheses have been advanced to explain the specific toxicity to the immune system in ADA deficiency. The apparently selective accumulation of dATP in thymocytes and peripheral blood B cells, with resultant inhibition of ribonucleotide reductase and DNA synthesis is probably the principal mechanism.

The structural gene for ADA is encoded as a single 32 kb locus containing 12 exons. Studies of the molecular defect in ADA-deficient patients have shown that mRNA is usually detectable in normal or supranormal amounts. Specific base substitution mutations have been detected in the majority of cases with the complete deficiency. A C-to-T base substitution mutation in exon 11 accounts for a high proportion of these, whilst a few patients are homozygous for large deletions encompassing exon I. A common point mutation resulting in a heat-labile ADA has been characterised in some patients with partial ADA deficiency, a disorder with an apparently increased prevalence in the Caribbean.

As yet no totally effective therapy for ADA deficiency has been reported, except in those few cases where bone marrow from an HLA/MLR compatible sibling donor was available.

Two therapeutic approaches have provided long-term benefit in specific instances. First, reconstitution using T cell depleted mismatched sibling marrow has been encouraging, particularly in early presenters completely deficient in ADA. Secondly, therapy with polyethylene glycol-modified adenosine deaminase (PEG-ADA) for more than 5 years has produced a sustained increase in lymphocyte numbers and mitogen responses together with evidence of in vivo B cell function. Success has generally been achieved in late presenters with residual ADA activity in mononuclear cells.

ADA deficiency has been chosen as the candidate disease for gene replacement therapy and the first human experiment commenced in 1990. The clinical consequences of overexpression of ADA activity - one of the potential hazards of gene implant - are known and take the form of an hereditary haemolytic anaemia associated with a tissue-specific increase in ADA activity. The genetic basis for the

latter autosomal dominant disorder seemingly relates to markedly increased levels of structurally normal ADA mRNA.

Table 10
ADA Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLN3TERM CAG to TAG	AGAGACCCACCGAGCGGCGGCGGAGGGAGCAGCGCCGGGG CGCACGAGGGCACCATGGCC**C**AGACGCCCGCCTTCGACAAG CCCAAAGTGAGCGCGCGCGGGGGCTCCGGGGACGGGGGTC	1
	GACCCCCGTCCCCGGAGCCCCCGCGCGCGCTCACTTTGGG CTTGTCGAAGGCGGGCGTCT**G**GGCCATGGTGCCCTCGTGCG CCCCGGCGCTGCTCCCTCCGCCGCCGCTCGGTGGGTCTCT	2
	CCATGGCC**C**AGACGCCC	3
	GGGCGTCT**G**GGCCATGG	4
Adenosine deaminase deficiency HIS15ASP CAT to GAT	TATTTGTTCTCTCTCTCCCTTTCTCTCTCTCTTCCCCCTGCCC CCTTGCAGGTAGAACTG**C**ATGTCCACCTAGACGGATCCATCA AGCCTGAAACCATCTTATACTATGGCAGGTAAGTCC	5
	GGACTTACCTGCCATAGTATAAGATGGTTTCAGGCTTGATGGA TCCGTCTAGGTGGACAT**G**CAGTTCTACCTGCAAGGGGGCAG GGGGAAGAGAGAGAGAAAGGGAGAGAGAGAACAAATA	6
	TAGAACTG**C**ATGTCCAC	7
	GTGGACAT**G**CAGTTCTA	8
Adenosine deaminase deficiency GLY20ARG GGA to AGA	TCCCTTTCTCTCTCTCTTCCCCCTGCCCCCTTGCAGGTAGAA CTGCATGTCCACCTAGAC**G**GATCCATCAAGCCTGAAACCATC TTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCT	9
	AGGGCTCTTCTGTATGGACTTACCTGCCATAGTATAAGATGGT TTCAGGCTTGATGGATC**C**GTCTAGGTGGACATGCAGTTCTAC CTGCAAGGGGGCAGGGGGAAGAGAGAGAGAAAGGGA	10
	ACCTAGAC**G**GATCCATC	11
	GATGGATC**C**GTCTAGGT	12
Adenosine deaminase deficiency GLY74CYS GGC to TGC	CCTGGAGCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACC CCTTTCTTCCCTTCCCAGG**G**GCTGCCGGGAGGCTATCAAAAG GATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGG	13

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCTTTT GATAGCCTCCCGGCAGC**<u>C</u>**CCTGGGAAGGGAAGAAAGGGGTT GGGAACAACCTTCCCCAAGTCCCTTGGGAGCTCCAGG	14
	CTATCGCG**<u>G</u>**GCTGCCGG	15
	CCGGCAGC**<u>C</u>**CGCGATAG	16
Adenosine Deaminase Deficiency ARG76TRP CGG to TGG	GCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACCCCTTTCT TCCCTTCCCAGGGGCTGC**<u>C</u>**GGGAGGCTATCAAAAGGATCGC CTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGG	17
	CCACGCCCTCTTTGGCCTTCATCTCTACAAACTCATAGGCGAT CCTTTTGATAGCCTCCC**<u>G</u>**GCAGCCCCTGGGAAGGGAAGAAA GGGGTTGGGAACAACCTTCCCCAAGTCCCTTGGGAGC	18
	GGGGCTGC**<u>C</u>**GGGAGGCT	19
	AGCCTCCC**<u>G</u>**GCAGCCCC	20
Adenosine Deaminase Deficiency LYS80ARG AAA to AGA	TTGGGGAAGGTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGG GCTGCCGGGAGGCTATCA**<u>A</u>**AAGGATCGCCTATGAGTTTGTAG AGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGT	21
	ACCTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTACAA ACTCATAGGCGATCCTT**<u>T</u>**TGATAGCCTCCCGGCAGCCCCTGG GAAGGGAAGAAAGGGGTTGGGAACAACCTTCCCCAA	22
	GGCTATCA**<u>A</u>**AAGGATCG	23
	CGATCCTT**<u>T</u>**TGATAGCC	24
Adenosine deaminase deficiency ALA83ASP GCC to GAC	GTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGGGCTGCCGGG AGGCTATCAAAAGGATCG**<u>C</u>**CTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGTATGTGGAGGTGCGGTACAG	25
	CTGTACCGCACCTCCACATACACCACGCCCTCTTTGGCCTTC ATCTCTACAAACTCATAG**<u>G</u>**CGATCCTTTTGATAGCCTCCCGGC AGCCCCTGGGAAGGGAAGAAAGGGGTTGGGAACAAC	26
	AAGGATCG**<u>C</u>**CTATGAGT	27
	ACTCATAG**<u>G</u>**CGATCCTT	28
Adenosine deaminase deficiency TYR97CYS TAT to TGT	AGGCTATCAAAAGGATCGCCTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGT**<u>A</u>**TGTGGAGGTGCGGTACAGTCCG CACCTGCTGGCCAACTCCAAAGTGGAGCCAATCCCCTG	29
	CAGGGGATTGGCTCCACTTTGGAGTTGGCCAGCAGGTGCGG ACTGTACCGCACCTCCACA**<u>T</u>**ACACCACGCCCTCTTTGGCCTT CATCTCTACAAACTCATAGGCGATCCTTTTGATAGCCT	30

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTGGTGT**A**TGTGGAGG	31
	CCTCCACA**T**ACACCACG	32
Adenosine deaminase deficiency ARG101GLN CGG to CAG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGC**G**GTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	33
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTAC**C**GCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC	34
	GGAGGTGC**G**GTACAGTC	35
	GACTGTAC**C**GCACCTCC	36
Adenosine deaminase deficiency ARG101LEU CGG to CTG	GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGC**G**GTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA	37
	TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTAC**C**GCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC	38
	GGAGGTGC**G**GTACAGTC	39
	GACTGTAC**C**GCACCTCC	40
Adenosine deaminase deficiency ARG101TRP CGG to TGG	AGGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGC GTGGTGTATGTGGAGGTG**C**GGTACAGTCCGCACCTGCTGGC CAACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTG	41
	CAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCCA GCAGGTGCGGACTGTACC**G**CACCTCCACATACACCACGCCC TCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCT	42
	TGGAGGTG**C**GGTACAGT	43
	ACTGTACC**G**CACCTCCA	44
Adenosine deaminase deficiency PRO104LEU CCG to CTG	ATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATG TGGAGGTGCGGTACAGTC**C**GCACCTGCTGGCCAACTCCAAA GTGGAGCCAATCCCCTGGAACCAGGCTGAGTGAGTGAT	45
	ATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCACTTTG GAGTTGGCCAGCAGGTGC**G**GACTGTACCGCACCTCCACATA CACCACGCCCTCTTTGGCCTTCATCTCTACAAACTCAT	46
	GTACAGTC**C**GCACCTGC	47
	GCAGGTGC**G**GACTGTAC	48

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency LEU106VAL CTG to GTG	TTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAG GTGCGGTACAGTCCGCAC**C**TGCTGGCCAACTCCAAAGTGGA GCCAATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCC	49
	GGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCA CTTTGGAGTTGGCCAGCA**G**GTGCGGACTGTACCGCACCTCC ACATACACCACGCCCTCTTTGGCCTTCATCTCTACAAA	50
	GTCCGCAC**C**TGCTGGCC	51
	GGCCAGCA**G**GTGCGGAC	52
Adenosine deaminase deficiency LEU107PRO CTG to CCG	TAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGTG CGGTACAGTCCGCACCTGC**T**GGCCAACTCCAAAGTGGAGCC AATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCCTGGA	53
	TCCAGGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGC TCCACTTTGGAGTTGGCC**A**GCAGGTGCGGACTGTACCGCAC CTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTA	54
	GCACCTGC**T**GGCCAACT	55
	AGTTGGCC**A**GCAGGTGC	56
Adenosine deaminase deficiency PRO126GLN CCA to CAA	GCCTTCCTTTTGCCTCAGGCCCATCCCTACTCCTCTCCTCAC ACAGAGGGGACCTCACCC**C**AGACGAGGTGGTGGCCCTAGTG GGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGT	57
	ACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCCAC TAGGGCCACCACCTCGTCT**G**GGGTGAGGTCCCCTCTGTGTG AGGAGAGGAGTAGGGATGGGCCTGAGGCAAAAGGAAGGC	58
	CCTCACCC**C**AGACGAGG	59
	CCTCGTCT**G**GGGTGAGG	60
Adenosine deaminase deficiency VAL129MET GTG to ATG	TTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACACAGAGGG GACCTCACCCCAGACGAG**G**TGGTGGCCCTAGTGGGCCAGGG CCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCC	61
	GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCC TGGCCCACTAGGGCCACCA**C**CTCGTCTGGGGTGAGGTCCCC TCTGTGTGAGGAGAGGAGTAGGGATGGGCCTGAGGCAAA	62
	CAGACGAG**G**TGGTGGCC	63
	GGCCACCA**C**CTCGTCTG	64

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency GLY140GLU GGG to GAG	ACAGAGGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGG**G**GGAGCGAGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAG	65
	CTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTCGCTCC**C**CCTCCTGCAGGCCCTGGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGT	66
	GCAGGAGG**G**GGAGCGAG	67
	CTCGCTCC**C**CCTCCTGC	68
Adenosine deaminase deficiency ARG142GLN CGA to CAA	GGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGC**G**AGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTA	69
	TACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCT**C**GCTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCC	70
	GGGGGAGC**G**AGACTTCG	71
	CGAAGTCT**C**GCTCCCCC	72
Adenosine deaminase deficiency ARG142TERM CGA to TGA	GGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAG**C**GAGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGT	73
	ACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTC**G**CTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCC	74
	AGGGGGAG**C**GAGACTTC	75
	GAAGTCTC**G**CTCCCCCT	76
Adenosine deaminase deficiency ARG149GLN CGG to CAG	TGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCC**G**GTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCCAGGG	77
	CCCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGAC**C**GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCA	78
	CAAGGCCC**G**GTCCATCC	79
	GGATGGAC**C**GGGCCTTG	80

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG149TRP CGG to TGG	GTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGC GAGACTTCGGGGTCAAGGCC**C**GGTCCATCCTGTGCTGCATG CGCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCCAGG	81
	CCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCGC ATGCAGCACAGGATGGACC**G**GGCCTTGACCCCGAAGTCTCG CTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCAC	82
	TCAAGGCC**C**GGTCCATC	83
	GATGGACC**G**GGCCTTGA	84
Adenosine deaminase deficiency LEU152MET CTG to ATG	CTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCG GGGTCAAGGCCCGGTCCATC**C**TGTGCTGCATGCGCCACCAG CCCAGTGAGTAGGATCACCGCCCTGCCCAGGGCCGCCCGT	85
	ACGGGCGGCCCTGGGCAGGGCGGTGATCCTACTCACTGGG CTGGTGGCGCATGCAGCACA**G**GATGGACCGGGCCTTGACCC CGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCCACTAG	86
	GGTCCATC**C**TGTGCTGC	87
	GCAGCACA**G**GATGGACC	88
Adenosine deaminase deficiency ARG156CYS CGC to TGC	GGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCC GGTCCATCCTGTGCTGCATG**C**GCCACCAGCCCAGTGAGTAG GATCACCGCCCTGCCCAGGGCCGCCCGTCTCACCCTGGCC	89
	GGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGATC CTACTCACTGGGCTGGTGGC**G**CATGCAGCACAGGATGGACC GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC	90
	GCTGCATG**C**GCCACCAG	91
	CTGGTGGC**G**CATGCAGC	92
Adenosine deaminase deficiency ARG156HIS CGC to CAC	GCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCCG GTCCATCCTGTGCTGCATGC**G**CCACCAGCCCAGTGAGTAGG ATCACCGCCCTGCCCAGGGCCGCCCGTCTCACCCTGGCCC	93
	GGGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGAT CCTACTCACTGGGCTGGTGG**C**GCATGCAGCACAGGATGGAC CGGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGC	94
	CTGCATGC**G**CCACCAGC	95
	GCTGGTGG**C**GCATGCAG	96

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency VAL177MET GTG to ATG	CTGCCCACAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAA GAAGTACCAGCAGCAGACC**G**TGGTAGCCATTGACCTGGCTG GAGATGAGACCATCCCAGGAAGCAGCCTCTTGCCTGGAC	97
	GTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCATCTCCAG CCAGGTCAATGGCTACCA**C**GGTCTGCTGCTGGTACTTCTTAC ACAGCTCCACCACCTTGGGGGACCAGTCTGTGGGCAG	98
	AGCAGACC**G**TGGTAGCC	99
	GGCTACCA**C**GGTCTGCT	100
Adenosine deaminase deficiency ALA179ASP GCC to GAC	CAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAAGAAGTAC CAGCAGCAGACCGTGGTAG**C**CATTGACCTGGCTGGAGATGA GACCATCCCAGGAAGCAGCCTCTTGCCTGGACATGTCCA	101
	TGGACATGTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCA TCTCCAGCCAGGTCAATG**G**CTACCACGGTCTGCTGCTGGTAC TTCTTACACAGCTCCACCACCTTGGGGGACCAGTCTG	102
	CGTGGTAG**C**CATTGACC	103
	GGTCAATG**G**CTACCACG	104
Adenosine deaminase deficiency GLN199PRO CAG to CCG	CCATTGACCTGGCTGGAGATGAGACCATCCCAGGAAGCAGC CTCTTGCCTGGACATGTCC**A**GGCCTACCAGGTGGGTCCTGT GAGAAGGAATGGAGAGGCTGGCCCTGGGTGAGCTTGTCT	105
	AGACAAGCTCACCCAGGGCCAGCCTCTCCATTCCTTCTCACA GGACCCACCTGGTAGGCC**T**GGACATGTCCAGGCAAGAGGCT GCTTCCTGGGATGGTCTCATCTCCAGCCAGGTCAATGG	106
	ACATGTCC**A**GGCCTACC	107
	GGTAGGCC**T**GGACATGT	108
Adenosine deaminase deficiency ARG211CYS CGT to TGT	GCTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGC TGTGAAGAGCGGCATTCAC**C**GTACTGTCCACGCCGGGGAGG TGGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGG	109
	CCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCCACCT CCCCGGCGTGGACAGTAC**G**GTGAATGCCGCTCTTCACAGCC TCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAGC	110
	GCATTCAC**C**GTACTGTC	111
	GACAGTAC**G**GTGAATGC	112

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency ARG211HIS CGT to CAT	CTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGCT GTGAAGAGCGGCATTCACC**G**TACTGTCCACGCCGGGGAGGT GGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGGC	113
	GCCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCCACC TCCCCGGCGTGGACAGTA**C**GGTGAATGCCGCTCTTCACAGC CTCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAG	114
	CATTCACC**G**TACTGTCC	115
	GGACAGTA**C**GGTGAATG	116
Adenosine deaminase deficiency ALA215THR GCC to ACC	ATGACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGG CATTCACCGTACTGTCCAC**G**CCGGGGAGGTGGGCTCGGCCG AAGTAGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGG	117
	CCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTACTTCGG CCGAGCCCACCTCCCCGG**C**GTGGACAGTACGGTGAATGCCG CTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGTCAT	118
	CTGTCCAC**G**CCGGGGAG	119
	CTCCCCGG**C**GTGGACAG	120
Adenosine deaminase deficiency GLY216ARG GGG to AGG	ACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCAT TCACCGTACTGTCCACGCC**G**GGGAGGTGGGCTCGGCCGAAG TAGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCC	121
	GGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTACTT CGGCCGAGCCCACCTCCC**C**GGCGTGGACAGTACGGTGAATG CCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGT	122
	TCCACGCC**G**GGGAGGTG	123
	CACCTCCC**C**GGCGTGGA	124
Adenosine deaminase deficiency GLU217LYS GAG to AAG	TGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATTCA CCGTACTGTCCACGCCGGG**G**AGGTGGGCTCGGCCGAAGTAG TAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCCCTC	125
	GAGGGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTA CTTCGGCCGAGCCCACCT**C**CCCGGCGTGGACAGTACGGTGA ATGCCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCA	126
	ACGCCGGG**G**AGGTGGGC	127
	GCCCACCT**C**CCCGGCGT	128

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency THR233ILE ACA to ATA	CTGCCTCCTCCCATACTTGGCTCTATTCTGCTTCTCTACAGGC TGTGGACATACTCAAGA**C**AGAGCGGCTGGGACACGGCTACC ACACCCTGGAAGACCAGGCCCTTTATAACAGGCTGCG	129
	CGCAGCCTGTTATAAAGGGCCTGGTCTTCCAGGGTGTGGTAG CCGTGTCCCAGCCGCTCT**G**TCTTGAGTATGTCCACAGCCTGT AGAGAAGCAGAATAGAGCCAAGTATGGGAGGAGGCAG	130
	ACTCAAGA**C**AGAGCGGC	131
	GCCGCTCT**G**TCTTGAGT	132
Adenosine deaminase deficiency ARG253PRO CGG to CCG	CAGAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAG GCCCTTTATAACAGGCTGC**G**GCAGGAAAACATGCACTTCGAG GTAAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGC	133
	GCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCTC GAAGTGCATGTTTTCCTGC**C**GCAGCCTGTTATAAAGGGCCTG GTCTTCCAGGGTGTGGTAGCCGTGTCCCAGCCGCTCTG	134
	CAGGCTGC**G**GCAGGAAA	135
	TTTCCTGC**C**GCAGCCTG	136
Adenosine deaminase deficiency GLN254TERM CAG to TAG	GAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAGGC CCTTTATAACAGGCTGCGG**C**AGGAAAACATGCACTTCGAGGT AAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGCTG	137
	CAGCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACC TCGAAGTGCATGTTTTCCT**G**CCGCAGCCTGTTATAAAGGGCC TGGTCTTCCAGGGTGTGGTAGCCGTGTCCCAGCCGCTC	138
	GGCTGCGG**C**AGGAAAAC	139
	GTTTTCCT**G**CCGCAGCC	140
Adenosine deaminase deficiency PRO274LEU CCG to CTG	CCACACACCTGCTCTTCCAGATCTGCCCCTGGTCCAGCTACC TCACTGGTGCCTGGAAGC**C**GGACACGGAGCATGCAGTCATT CGGTGAGCTCTGTTCCCCTGGGCCTGTTCAATTTTGTT	141
	AACAAAATTGAACAGGCCCAGGGGAACAGAGCTCACCGAATG ACTGCATGCTCCGTGTCC**G**GCTTCCAGGCACCAGTGAGGTA GCTGGACCAGGGGCAGATCTGGAAGAGCAGGTGTGTGG	142
	CTGGAAGC**C**GGACACGG	143
	CCGTGTCC**G**GCTTCCAG	144

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenosine deaminase deficiency SER291LEU TCG to TTG	GGAGGCTGATTCTCTCCTCCTCCCTCTTCTGCAGGCTCAAAAATGACCAGGCTAACTACT**C**GCTCAACACAGATGACCCGCTCATCTTCAAGTCCACCCTGGACACTGATTACCAGATGAC	145
	GTCATCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGCGGGTCATCTGTGTTGAGC**G**AGTAGTTAGCCTGGTCATTTTTGAGCCTGCAGAAGAGGGAGGAGGAGAGAATCAGCCTCC	146
	TAACTACT**C**GCTCAACA	147
	TGTTGAGC**G**AGTAGTTA	148
Adenosine deaminase deficiency PRO297GLN CCG to CAG	CCTCCCTCTTCTGCAGGCTCAAAAATGACCAGGCTAACTACTCGCTCAACACAGATGACC**C**GCTCATCTTCAAGTCCACCCTGGACACTGATTACCAGATGACCAAACGGGACATGGGCTT	149
	AAGCCCATGTCCCGTTTGGTCATCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGC**G**GGTCATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTTTGAGCCTGCAGAAGAGGGAGG	150
	AGATGACC**C**GCTCATCT	151
	AGATGAGC**G**GGTCATCT	152
Adenosine deaminase deficiency LEU304ARG CTG to CGG	AAAATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGCTCATCTTCAAGTCCACCC**T**GGACACTGATTACCAGATGACCAAACGGGACATGGGCTTTACTGAAGAGGAGTTTAAAAG	153
	CTTTTAAACTCCTCTTCAGTAAAGCCCATGTCCCGTTTGGTCATCTGGTAATCAGTGTCC**A**GGGTGGACTTGAAGATGAGCGGGTCATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTT	154
	GTCCACCC**T**GGACACTG	155
	CAGTGTCC**A**GGGTGGAC	156
Adenosine deaminase deficiency ALA329VAL C-to-T at base 1081	GCCTTCTTTGTTCTCTGGTTCCATGTTGTCTGCCATTCTGGCCTTTCCAGAACATCAATG**C**GGCCAAATCTAGTTTCCTCCCAGAAGATGAAAAGAGGGAGCTTCTCGACCTGCTCTATAA	157
	TTATAGAGCAGGTCGAGAAGCTCCCTCTTTTCATCTTCTGGGAGGAAACTAGATTTGGCC**G**CATTGATGTTCTGGAAAGGCCAGAATGGCAGACAACATGGAACCAGAGAACAAAGAAGGC	158
	CATCAATG**C**GGCCAAAT	159
	ATTTGGCC**G**CATTGATG	160

EXAMPLE 5
P53 Mutations

The p53 gene codes for a protein that acts as a transcription factor and serves as a key regulator of the cell cycle. Mutation in this gene is probably the most significant genetic change characterizing the transformation of cells from normalcy to malignancy.

Inactivation of p53 by mutation disrupts the cell cycle which, in turn, sets the stage for tumor formation. Mutations in the p53 gene are among the most commonly diagnosed genetic disorders, occuring in as many as 50% of cancer patients. For some types of cancer, most notably of the breast, lung and colon, p53 mutations are the predominant genetic alternations found thus far. These mutations are associated with genomic instability and thus an increased susceptibility to cancer. Some p53 lesions result in malignancies that are resistant to the most widely used therapeutic regimens and therefore demand more aggressive treatment.

That p53 is associated with different malignant tumors is illustrated in the Li-Fraumeni autosomal dominant hereditary disorder characterized by familial multiple tumors due to mutation in the p53 gene. Affected individuals can develop one or more tumors, including: brain (12%); soft-tissue sarcoma (12%); breast cancer (25%); adrenal tumors (1%); bone cancer (osteosarcoma) (6%); cancer of the lung, prostate, pancreas, and colon as well as lymphoma and melanoma can also occur.

Certain of the most frequently mutated codons are codons 175, 248 and 273, however a variety of oligonucleotides are described below in the atttached table.

Table 11
p53 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
In 2 families with Li-Fraumeni syndrome, there was a C-to-T mutation at the first nucleotide of codon 248 which changed arginine to tryptophan.	GACTGTACCACCATCCACTACAACTACATGTGTAACAGTTCCT GCATGGGCGGCATGAAC<u>C</u>GGAGGCCCATCCTCACCATCATC ACACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACC	161
	GGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGA TGGTGAGGATGGGCCTCC<u>G</u>GTTCATGCCGCCCATGCAGGAA CTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC	162
	GCATGAAC<u>C</u>GGAGGCCC	163

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
-	GGGCCTCC**G**GTTCATGC	164
In a family with the Li-Fraumeni syndrome, a G-to-A mutation at the first nucleotide of codon 258 resulting in the substitution of lysine for glutamic acid.	TGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCAT CCTCACCATCATCACACTG**G**AAGACTCCAGGTCAGGAGCCAC TTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTC	165
	GAGGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGT GGCTCCTGACCTGGAGTCTT**C**CAGTGTGATGATGGTGAGGAT GGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACA	166
	TCACACTG**G**AAGACTCC	167
	GGAGTCTT**C**CAGTGTGA	168
In a family with the Li-Fraumeni syndrome, a G-to-T mutation at the first nucleotide of codon 245 resulting in the substitution of cysteine for glycine.	GTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTA ACAGTTCCTGCATGGGC**G**GCATGAACCGGAGGCCCATCCTC ACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCA	169
A gly245-to-ser, GGC-to-AGC, mutation was found in a patient in whom osteosarcoma was diagnosed at the age of 18 years.	TGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGA TGGGCCTCCGGTTCATGC**C**GCCCATGCAGGAACTGTTACACA TGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAAC	170
	GCATGGGC**G**GCATGAAC	171
	GTTCATGC**C**GCCCATGC	172
In a family with the Li-Fraumeni syndrome, a germline mutation at codon 252: a T-to-C change at the second position resulted in substitution of proline for leucine.	TCCACTACAACTACATGTGTAACAGTTCCTGCATGGGCGGCA TGAACCGGAGGCCCATCC**T**CACCATCATCACACTGGAAGACT CCAGGTCAGGAGCCACTTGCCACCCTGCACACTGGCC	173
	GGCCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTC TTCCAGTGTGATGATGGTG**A**GGATGGGCCTCCGGTTCATGCC GCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGA	174
	GCCCATCC**T**CACCATCA	175
	TGATGGTG**A**GGATGGGC	176

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Researchers analyzed for mutations in p53 hepatocellular carcinomas from patients in Qidong, an area of high incidence in China, in which both hepatitis B virus and aflatoxin B1 are risk factors. Eight of 16 tumors had a point mutation at the third base position of codon 249. The G-to-T mutation at codon 249 led to a change from arginine to serine (AGG to AGT).	TACCACCATCCACTACAACTACATGTGTAACAGTTCCTGCATG GGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACT GGAAGACTCCAGGTCAGGAGCCACTTGCCACCCTGCA	177
	TGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTG TGATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATG CAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTA	178
	AACCGGAGGCCCATCCT	179
	AGGATGGGCCTCCGGTT	180
In cases of hepatocellular carcinoma in southern Africa, a G-to-T substitution in codon 157 resulting in a change from valine to phenylalanine.	CTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACA CCCCCGCCCGGCACCCGCGTCCGCGCCATGGCCATCTACAA GCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCC	181
	GGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGT AGATGGCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGT GGAATCAACCCACAGCTGCACAGGGCAGGTCTTGGCCAG	182
	GCACCCGCGTCCGCGCC	183
	GGCGCGGACGCGGGTGC	184
In a family with Li-Fraumeni in which noncancerous skin fibroblasts from affected individuals showed an unusual radiation-resistant phenotype, a point mutation in codon 245 of the P53 gene. A change from GGC to GAC predicted substitution of aspartic acid for glycine.	TTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAA CAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA CCATCATCACACTGGAAGACTCCAGGTCAGGAGCCAC	185
	GTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGG ATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACAC ATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAA	186
	CATGGGCGGCATGAACC	187
	GGTTCATGCCGCCCATG	188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
In 2 of 8 families with Li-Fraumeni syndrome, a mutation in codon 248: a CGG-to-CAG change resulting in substitution of glutamine for arginine.	ACTGTACCACCATCCACTACAACTACATGTGTAACAGTTCCTG CATGGGCGGCATGAACC**G**GAGGCCCATCCTCACCATCATCA CACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACCC	189
	GGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGAT GATGGTGAGGATGGGCCTC**C**GGTTCATGCCGCCCATGCAGG AACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGT	190
	CATGAACC**G**GAGGCCCA	191
	TGGGCCTC**C**GGTTCATG	192
In 9 members of an extended family with Li-Fraumeni syndrome, a germline mutation at codon 133 (ATG-to-ACG), resulted in the substitution of threonine for methionine (M133T), and completely cosegregated with the cancer syndrome.	CCCTGACTTTCAACTCTGTCTCCTTCCTCTTCCTACAGTACTC CCCTGCCCTCAACAAGA**T**GTTTTGCCAACTGGCCAAGACCTG CCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCC	193
	GGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGT CTTGGCCAGTTGGCAAAAC**A**TCTTGTTGAGGGCAGGGGAGTA CTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGG	194
	CAACAAGA**T**GTTTTGCC	195
	GGCAAAAC**A**TCTTGTTG	196
In 1 pedigree consistent with the Li-Fraumeni syndrome, a germline G-to-T transversion at codon 272 (valine to leucine) was found.	TCTTGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGG GACGGAACAGCTTTGAG**G**TGCGTGTTTGTGCCTGTCCTGGGA GAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGA	197
	TCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAG GACAGGCACAAACACGCA**C**CTCAAAGCTGTTCCGTCCCAGTA GATTACCACTACTCAGGATAGGAAAAGAGAAGCAAGA	198
	GCTTTGAG**G**TGCGTGTT	199
	AACACGCA**C**CTCAAAGC	200
A ser241-to-phe mutation due to a TCC-to-TTC change was found in a patient with hepatoblastoma and multiple foci of osteosarcoma	TTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACAA CTACATGTGTAACAGTT**C**CTGCATGGGCGGCATGAACCGGAG GCCCATCCTCACCATCATCACACTGGAAGACTCCAG	201
	CTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCCG GTTCATGCCGCCCATGCAG**G**AACTGTTACACATGTAGTTGTA GTGGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAA	202

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAACAGTT**C**CTGCATGG	203
	CCATGCAG**G**AACTGTTA	204
An AAG-to-TAG change of codon 120, resulting in conversion from lysine to a stop codon, was found in a patient with osteosarcoma and adenocarcinoma of the lung at age 18 and brain tumor (glioma) at the age of 27.	CAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTC TTGCATTCTGGGACAGCC**A**AGTCTGTGACTTGCACGGTCAGT TGCCCTGAGGGGCTGGCTTCCATGAGACTTCAATGCC	205
	GGCATTGAAGTCTCATGGAAGCCAGCCCCTCAGGGCAACTG ACCGTGCAAGTCACAGACT**T**GGCTGTCCCAGAATGCAAGAAG CCCAGACGGAAACCGTAGCTGCCCTGGTAGGTTTTCTG	206
	GGACAGCC**A**AGTCTGTG	207
	CACAGACT**T**GGCTGTCC	208
A CGG-to-TGG change at codon 282, resulting in the substitution of tryptophan for arginine, was found in a patient who developed osteosarcoma at the age of 10 years.	GGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGT GCCTGTCCTGGGAGAGAC**C**GGCGCACAGAGGAAGAGAATCT CCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCCAG	209
	CTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGA TTCTCTTCCTCTGTGCGCC**G**GTCTCTCCCAGGACAGGCACAA ACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACC	210
	GGAGAGAC**C**GGCGCACA	211
	TGTGCGCC**G**GTCTCTCC	212
In 5 of 6 anaplastic carcinomas of the thyroid and in an anaplastic carcinoma thyroid cell line ARO, a CGT-to-CAT mutation converted arginine-273 to histidine.	GCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACG GAACAGCTTTGAGGTGC**G**TGTTTGTGCCTGTCCTGGGAGAGA CCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGG	213
	CCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTC CCAGGACAGGCACAAACA**C**GCACCTCAAAGCTGTTCCGTCCC AGTAGATTACCACTACTCAGGATAGGAAAAGAGAAGC	214
	TGAGGTGC**G**TGTTTGTG	215
	CACAAACA**C**GCACCTCA	216

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
A germline GGA-to-GTA mutation resulting in a change of glycine-325 to valine was found in a patient who had non-Hodgkin lymphoma diagnosed at age 17 and colon carcinoma at age 26.	TCCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAA AGAAGAAACCACTGGATG**G**AGAATATTTCACCCTTCAGGTACT AAGTCTTGGGACCTCTTATCAAGTGGAAAGTTTCCA	217
	TGGAAACTTTCCACTTGATAAGAGGTCCCAAGACTTAGTACCT GAAGGGTGAAATATTCT**C**CATCCAGTGGTTTCTTCTTTGGCTG GGGAGAGGAGCTGGTGTTGTTGGGCAGTGCTAGGA	218
	ACTGGATG**G**AGAATATT	219
	AATATTCT**C**CATCCAGT	220
CGC-CCC Arg-72 to Pro association with Lung cancer	AATGGTTCACTGAAGACCCAGGTCCAGATGAAGCTCCCAGAA TGCCAGAGGCTGCTCCCC**G**CGTGGCCCCTGCACCAGCAGCT CCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCC	221
	GGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAG CTGCTGGTGCAGGGGCCACG**C**GGGGAGCAGCCTCTGGCATT CTGGGAGCTTCATCTGGACCTGGGTCTTCAGTGAACCATT	222
	TGCTCCCC**G**CGTGGCCC	223
	GGGCCACG**C**GGGGAGCA	224
CCG-CTG Pro-82 to Leu Breast cancer	AAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCT GCACCAGCAGCTCCTACAC**C**GGCGGCCCCTGCACCAGCCCC CTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAGAAAAC	225
	GTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGG GGCTGGTGCAGGGGCCGCC**G**GTGTAGGAGCTGCTGGTGCA GGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTT	226
	TCCTACAC**C**GGCGGCCC	227
	GGGCCGCC**G**GTGTAGGA	228
cCAA-TAA Gln-136 to Term Li-Fraumeni syndrome	TTCAACTCTGTCTCCTTCCTCTTCCTACAGTACTCCCCTGCCC TCAACAAGATGTTTTGC**C**AACTGGCCAAGACCTGCCCTGTGC AGCTGTGGGTTGATTC**C**ACACCCCCGCCCGGCACCC	229
	GGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACA GGGCAGGTCTTGGCCAGTT**G**GCAAAACATCTTGTTGAGGGCA GGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTTGAA	230
	TGTTTTGC**C**AACTGGCC	231
	GGCCAGTT**G**GCAAAACA	232

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
TGC-TAC Cys-141 to Tyr Li-Fraumeni syndrome	TCCTCTTCCTACAGTACTCCCCTGCCCTCAACAAGATGTTTTG CCAACTGGCCAAGACCT**G**CCCTGTGCAGCTGTGGGTTGATTC **C**ACACCCCCGCCCGGCACCCGCGTCCGCGCCATGGC	233
	GCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAAT CAACCCACAGCTGCACAGGG**C**AGGTCTTGGCCAGTTGGCAA AACATCTTGTTGAGGGCAGGGGAGTACTGTAGGAAGAGGA	234
	CAAGACCT**G**CCCTGTGC	235
	GCACAGGG**C**AGGTCTTG	236
aCCC-TCC Pro-151 to Ser Li-Fraumeni syndrome	AACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAG CTGTGGGTTGATTC**C**ACA**C**CCCCGCCCGGCACCCGCGTCCG CGCCATGGCCATCTACAAGCAGTCACAGCACATGACGG	237
	CCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGG ACGCGGGTGCCGGGCGGGG**G**TGTGGAATCAACCCACAGCT GCACAGGGCAGGTCTTGGCCAGTTGGCAAAACATCTTGTT	238
	ATTCCACA**C**CCCCGCCC	239
	GGGCGGGG**G**TGTGGAAT	240
CCG-CTG Pro-152 to Leu Adrenocortical carcinoma	AGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGT GGGTTGATTC**C**ACACCCC**C**GCCCGGCACCCGCGTCCGCGCC ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGT	241
	ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCG CGGACGCGGGTGCCGGGC**G**GGGGTGTGGAATCAACCCACA GCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAAACATCT	242
	CACACCCC**C**GCCCGGCA	243
	TGCCGGGC**G**GGGGTGTG	244
GGC-GTC Gly-154 to Val Glioblastoma	TTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTG ATTC**C**ACACCCCCGCCCG**G**CACCCGCGTCCGCGCCATGGCC ATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAG	245
	CTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCC ATGGCGCGGACGCGGGTG**C**CGGGCGGGGGTGTGGAATCAA CCCACAGCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAA	246
	CCCGCCCG**G**CACCCGCG	247
	CGCGGGTG**C**CGGGCGGG	248
CGC-CAC Arg-175 to His Li-Fraumeni syndrome	CCCGCGTCCGCGCCATGGCCATCTACAAGCAGTCACAGCAC ATGACGGAGGTTGTGAGGC**G**CTGCCCCCACCATGAGCGCTG CTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACG	249

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTCTCTCCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAG CGCTCATGGTGGGGGCAG**C**GCCTCACAACCTCCGTCATGTG CTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGG	250
	TGTGAGGC**G**CTGCCCCC	251
	GGGGGCAG**C**GCCTCACA	252
tGAG-AAG Glu-180 to Lys Li-Fraumeni syndrome	ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTG AGGCGCTGCCCCCACCAT**G**AGCGCTGCTCAGATAGCGATGG TGAGCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGC	253
	GCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCACCAT CGCTATCTGAGCAGCGCT**C**ATGGTGGGGGCAGCGCCTCACA ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCAT	254
	CCCACCAT**G**AGCGCTGC	255
	GCAGCGCT**C**ATGGTGGG	256
gCGC-TGC Arg-181 to Cys Breast cancer	GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGG CGCTGCCCCCACCATGAG**C**GCTGCTCAGATAGCGATGGTGA GCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCCA	257
	TGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCA CCATCGCTATCTGAGCAGC**G**CTCATGGTGGGGGCAGCGCCT CACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGC	258
	ACCATGAG**C**GCTGCTCA	259
	TGAGCAGC**G**CTCATGGT	260
CGC-CAC Arg-81 to His Breast cancer	CCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGC GCTGCCCCCACCATGAGC**G**CTGCTCAGATAGCGATGGTGAG CAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCCAG	261
	CTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTC ACCATCGCTATCTGAGCAG**C**GCTCATGGTGGGGGCAGCGCC TCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGG	262
	CCATGAGC**G**CTGCTCAG	263
	CTGAGCAG**C**GCTCATGG	264
CAT-CGT His-193 to Arg Li-Fraumeni syndrome	CCAGGGTCCCCAGGCCTCTGATTCCTCACTGATTGCTCTTAG GTCTGGCCCCTCCTCAGC**A**TCTTATCCGAGTGGAAGGAAATT TGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCG	265
	CGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTC CTTCCACTCGGATAAGA**T**GCTGAGGAGGGGCCAGACCTAAGA GCAATCAGTGAGGAATCAGAGGCCTGGGGACCCTGG	266

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCTCAGC**A**TCTTATCC	267
	GGATAAGA**T**GCTGAGGA	268
cCGA-TGA Arg-196 to Term Adrenocortical carcinoma	CCCAGGCCTCTGATTCCTCACTGATTGCTCTTAGGTCTGGCCCCTCCTCAGCATCTTATC**C**GAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTG	269
	CACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTC**G**GATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAATCAGTGAGGAATCAGAGGCCTGGG	270
	ATCTTATC**C**GAGTGGAA	271
	TTCCACTC**G**GATAAGAT	272
cAGA-TGA Arg-209 to Term Li-Fraumeni syndrome	GCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGAC**A**GAAACACTTTTCGACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAA	273
	TTGCAAACCAGACCTCAGGCGGCTCATAGGGCACCACCACACTATGTCGAAAAGTGTTTC**T**GTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGC	274
	TGGATGAC**A**GAAACACT	275
	AGTGTTTC**T**GTCATCCA	276
tCGA-TGA Arg-213 to Term Li-Fraumeni syndrome	CATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTT**C**GACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAACTGGGGTCTCTG	277
	CAGAGACCCCAGTTGCAAACCAGACCTCAGGCGGCTCATAGGGCACCACCACACTATGTC**G**AAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATG	278
	ACACTTTT**C**GACATAGT	279
	ACTATGTC**G**AAAAGTGT	280
gCCC-TCC Pro-219 to Ser Adrenocortical carcinoma	GGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTG**C**CCTATGAGCCGCCTGAGGTCTGGTTTGCAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGT	281
	ACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAACCAGACCTCAGGCGGCTCATAGG**G**CACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCC	282
	TGGTGGTG**C**CCTATGAG	283
	CTCATAGG**G**CACCACCA	284

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
TAT-TGT Tyr-220 to Cys Li-Fraumeni syndrome	ATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACA TAGTGTGGTGGTGCCCT**A**TGAGCCGCCTGAGGTCTGGTTTG CAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTT	285
	AACCACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAAC CAGACCTCAGGCGGCTCA**T**AGGGCACCACCACACTATGTCG AAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAAT	286
	GGTGCCCT**A**TGAGCCGC	287
	GCGGCTCA**T**AGGGCACC	288
cTCT-ACT Ser-227 to Thr Rhabdomyosarcoma	CACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCCTG TGTTATCTCCTAGGTTGGC**T**CTGACTGTACCACCATCCACTAC AACTACATGTGTAACAGTTCCTGCATGGGCGGCATGA	289
	TCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGT GGATGGTGGTACAGTCAG**A**GCCAACCTAGGAGATAACACAG GCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCTGTG	290
	AGGTTGGC**T**CTGACTGT	291
	ACAGTCAG**A**GCCAACCT	292
cCAC-AAC His-233 to Asn Glioma	GCACTGGCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGC TCTGACTGTACCACCATC**C**ACTACAACTACATGTGTAACAGTT CCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA	293
	TGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTG TTACACATGTAGTTGTAGT**G**GATGGTGGTACAGTCAGAGCCA ACCTAGGAGATAACACAGGCCCAAGATGAGGCCAGTGC	294
	CCACCATC**C**ACTACAAC	295
	GTTGTAGT**G**GATGGTGG	296
cAAC-GAC Asn-235 to Asp Adrenocortical carcinoma	GCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGAC TGTACCACCATCCACTAC**A**ACTACATGTGTAACAGTTCCTGCA TGGGCGGCATGAACCGGAGGCCCATCCTCACCATCA	297
	TGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAG GAACTGTTACACATGTAGT**T**GTAGTGGATGGTGGTACAGTCA GAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGGC	298
	TCCACTAC**A**ACTACATG	299
	CATGTAGT**T**GTAGTGGA	300
AAC-AGC Asn-235 to Ser Rhabdomyosarcoma	CCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGACT GTACCACCATCCACTACA**A**CTACATGTGTAACAGTTCCTGCAT GGGCGGCATGAACCGGAGGCCCATCCTCACCATCAT	301

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCA GGAACTGTTACACATGTAG**T**TGTAGTGGATGGTGGTACAGTC AGAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGG	302
	CCACTACA**A**CTACATGT	303
	ACATGTAG**T**TGTAGTGG	304
ATCc-ATG Ile-251 to Met Glioma	CATCCACTACAACTACATGTGTAACAGTTCCTGCATGGGCGG CATGAACCGGAGGCCCAT**C**CTCACCATCATCACACTGGAAGA CTCCAGGTCAGGAGCCACTTGCCACCCTGCACACTGG	305
	CCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTT CCAGTGTGATGATGGTGAG**G**ATGGGCCTCCGGTTCATGCCG CCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATG	306
	AGGCCCAT**C**CTCACCAT	307
	ATGGTGAG**G**ATGGGCCT	308
ACA-ATA Thr-256 to Ile Glioblastoma	ACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGG CCCATCCTCACCATCATCA**C**ACTGGAAGACTCCAGGTCAGGA GCCACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCA	309
	TGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGGCTCC TGACCTGGAGTCTTCCAGT**G**TGATGATGGTGAGGATGGGCCT CCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGT	310
	CATCATCA**C**ACTGGAAG	311
	CTTCCAGT**G**TGATGATG	312
CTG-CAG Leu-257 to Gln Li-Fraumeni syndrome	TGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCC ATCCTCACCATCATCACAC**T**GGAAGACTCCAGGTCAGGAGCC ACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCC	313
	GGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGG CTCCTGACCTGGAGTCTTCC**A**GTGTGATGATGGTGAGGATGG GCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACA	314
	CATCACAC**T**GGAAGACT	315
	AGTCTTCC**A**GTGTGATG	316
CTG-CCG Leu-265 to Pro Li-Fraumeni syndrome	GACCTGATTTCCTTACTGCCTCTTGCTTCTCTTTTCCTATCCT GAGTAGTGGTAATCTAC**T**GGGACGGAACAGCTTTGAGGTGCG TGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGA	317
	TCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCAC CTCAAAGCTGTTCCGTCCC**A**GTAGATTACCACTACTCAGGAT AGGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTC	318

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATCTAC**T**GGGACGGA	319
	TCCGTCCC**A**GTAGATTA	320
gCGT-TGT Arg-273 to Cys Li-Fraumeni syndrome	TGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGAC GGAACAGCTTTGAGGTG**C**GTGTTTGTGCCTGTCCTGGGAGA GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAG	321
	CTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCC CAGGACAGGCACAAACAC**G**CACCTCAAAGCTGTTCCGTCCCA GTAGATTACCACTACTCAGGATAGGAAAAGAGAAGCA	322
	TTGAGGTG**C**GTGTTTGT	323
	ACAAACAC**G**CACCTCAA	324
TGT-TAT Cys-275 to Tyr Li-Fraumeni syndrome	CTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACA GCTTTGAGGTGCGTGTTT**G**TGCCTGTCCTGGGAGAGACCGG CGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCC	325
	GGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGG TCTCTCCCAGGACAGGCA**C**AAACACGCACCTCAAAGCTGTTC CGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAG	326
	GCGTGTTT**G**TGCCTGTC	327
	GACAGGCA**C**AAACACGC	328
CCT-CTT Pro-278 to Leu Breast cancer	TCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGG TGCGTGTTTGTGCCTGTC**C**TGGGAGAGACCGGCGCACAGAG GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGA	329
	TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCT GTGCGCCGGTCTCTCCCA**G**GACAGGCACAAACACGCACCTC AAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGA	330
	TGCCTGTC**C**TGGGAGAG	331
	CTCTCCCA**G**GACAGGCA	332
AGA-AAA Arg-280 to Lys Glioma	GTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTG TTTGTGCCTGTCCTGGGA**G**AGACCGGCGCACAGAGGAAGAG AATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCC	333
	GGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCT TCCTCTGTGCGCCGGTCT**C**TCCCAGGACAGGCACAAACACG CACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTAC	334
	TCCTGGGA**G**AGACCGGC	335
	GCCGGTCT**C**TCCCAGGA	336

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
GAA-GCA Glu-286 to Ala Adrenocortical carcinoma	GGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA GACCGGCGCACAGAGGAAG**A**GAATCTCCGCAAGAAAGGGGA GCCTCACCACGAGCTGCCCCCAGGGAGCACTAAGCGAGG	337
	CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTC CCCTTTCTTGCGGAGATTC**T**CTTCCTCTGTGCGCCGGTCTCT CCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCC	338
	AGAGGAAG**A**GAATCTCC	339
	GGAGATTC**T**CTTCCTCT	340
CGA-CCA Arg-306 to Pro Rhabdomyosarcoma	AAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTG CCCCCAGGGAGCACTAAGC**G**AGGTAAGCAAGCAGGACAAGA AGCGGTGGAGGAGACCAAGGGTGCAGTTATGCCTCAGAT	341
	ATCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCT TGTCCTGCTTGCTTACCT**C**GCTTAGTGCTCCCTGGGGGCAGC TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT	342
	CACTAAGC**G**AGGTAAGC	343
	GCTTACCT**C**GCTTAGTG	344
gCGA-TGA Arg-306 to Term Li-Fraumeni syndrome	GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCT GCCCCCAGGGAGCACTAAG**C**GAGGTAAGCAAGCAGGACAAG AAGCGGTGGAGGAGACCAAGGGTGCAGTTATGCCTCAGA	345
	TCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTT GTCCTGCTTGCTTACCTC**G**CTTAGTGCTCCCTGGGGGCAGCT CGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTC	346
	GCACTAAG**C**GAGGTAAG	347
	CTTACCTC**G**CTTAGTGC	348
gCGC-TGC Arg-337 to Cys Osteosarcoma	GGTACTGTGAATATACTTACTTCTCCCCCTCCTCTGTTGCTGC AGATCCGTGGGCGTGAG**C**GCTTCGAGATGTTCCGAGAGCTG AATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGA	349
	TCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTCAGCT CTCGGAACATCTCGAAGC**G**CTCACGCCCACGGATCTGCAGC AACAGAGGAGGGGGAGAAGTAAGTATATTCACAGTACC	350
	GGCGTGAG**C**GCTTCGAG	351
	CTCGAAGC**G**CTCACGCC	352
CTG-CCG Leu-344 to Pro Li-Fraumeni syndrome	CTCCCCCTCCTCTGTTGCTGCAGATCCGTGGGCGTGAGCGC TTCGAGATGTTCCGAGAGC**T**GAATGAGGCCTTGGAACTCAAG GATGCCCAGGCTGGGAAGGAGCCAGGGGGAGCAGGGC	353

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTT GAGTTCCAAGGCCTCATTCAGCTCTCGGAACATCTCGAAGCG CTCACGCCCACGGATCTGCAGCAACAGAGGAGGGGGAG	354
	CCGAGAGCTGAATGAGG	355
	CCTCATTCAGCTCTCGG	356

EXAMPLE 6
beta globin

Hemoglobin, the major protein in the red blood cell, binds oxygen reversibly and is responsible for the cells' capacity to transport oxygen to the tissues. In adults, the major hemoglobin is hemoglobin A, a tetrameric protein consisting of two identical alpha globin chains and two beta globin chains. Disorders involving hemoglobin are among the most common genetic disorders worldwide, with approximately 5% of the world's population being carriers for clinically important hemoglobin mutations. Approximately 300,000 severely affected homozygotes or compound heterozygotes are born each year.

Mutation of the glutamic acid at position 7 in beta globin to valine causes sickle cell anemia, the clinical manifestations of which are well known. Mutations that cause absence of beta chain cause beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. For clinical purposes, beta-thalassemia is divided into thalassemia major (transfusion dependent), thalassemia intermedia (of intermediate severity), and thalassemia minor (asymptomatic). Patients with thalassemia major present in the first year of life with severe anemia; they are unable to maintain a hemoglobin level about 5 gm/dl.

The beta-thalassemias were among the first human genetic diseases to be examined by means of recombinant DNA analysis. Baysal et al., *Hemoglobin* 19(3-4):213-36 (1995) and others provide a compendium of mutations that result in beta-thalassemia.

Hemoglobin disorders were among the first to be considered for gene therapy. Transcriptional silencing of genes transferred into hematopoietic stem cells, however, poses one of the most significant challenges to its success. If the transferred gene is not completely silenced, a progressive decline in gene expression is often observed. Position effect variegation (PEV) and silencing mechanisms may act on a transferred globin gene residing in chromatin outside of the normal globin locus during the important terminal phases of erythroblast development when globin transcripts normally

accumulate rapidly despite heterochromatization and shutdown of the rest of the genome. The attached table discloses the correcting oligonucleotide base sequences for the beta globin oligonucleotides of the invention.

Table 12
Beta Globin Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Sickle Cell Anemia GLU-7-VAL GAG to GTG	TCTGACACAACTGTGTTCACTAGCAACCTCAAACAGACACCA TGGTGCACCTGACTCCTG**A**GGAGAAGTCTGCCGTTACTGCC CTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA	357
	TCACCACCAACTTCATCCACGTTCACCTTGCCCCACAGGGCA GTAACGGCAGACTTCTCC**T**CAGGAGTCAGGTGCACCATGGT GTCTGTTTGAGGTTGCTAGTGAACACAGTTGTGTCAGA	358
	GACTCCTG**A**GGAGAAGT	359
	ACTTCTCC**T**CAGGAGTC	360
Thalassaemia Beta MET-0-ARG ATG to AGG	CTATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCA ACCTCAAACAGACACCA**T**GGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	361
	ACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACC**A**TGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	362
	AGACACCA**T**GGTGCACC	363
	GGTGCACC**A**TGGTGTCT	364
Thalassaemia Beta MET-0-ILE ATG to ATA	TATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCAA CCTCAAACAGACACCAT**G**GTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	365
	CACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCAC**C**ATGGTGTCTGTTTGAGGTTGC TAGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATA	366
	GACACCAT**G**GTGCACCT	367
	AGGTGCAC**C**ATGGTGTC	368
Thalassaemia Beta MET-0-ILE ATG to ATT	TATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCAA CCTCAAACAGACACCAT**G**GTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	369

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACC**C**ATGGTGTCTGTTTGAGGTTGC TAGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATA	370
	GACACCAT**G**GTGCACCT	371
	AGGTGCAC**C**ATGGTGTC	372
Thalassaemia Beta MET-0-LYS ATG to AAG	CTATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCA ACCTCAAACAGACACCA**T**GGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	373
	ACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACC**A**TGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	374
	AGACACCA**T**GGTGCACC	375
	GGTGCACC**A**TGGTGTCT	376
Thalassaemia Beta MET-0-THR ATG to ACG	CTATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGCA ACCTCAAACAGACACCA**T**GGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT	377
	ACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACC**A**TGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAG	378
	AGACACCA**T**GGTGCACC	379
	GGTGCACC**A**TGGTGTCT	380
Thalassaemia Beta MET-0-VAL ATG to GTG	TCTATTGCTTACATTTGCTTCTGACACAACTGTGTTCACTAGC AACCTCAAACAGACACC**A**TGGTGCACCTGACTCCTGAGGAG AAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACG	381
	CGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCC TCAGGAGTCAGGTGCACCA**T**GGTGTCTGTTTGAGGTTGCTAG TGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAGA	382
	CAGACACC**A**TGGTGCAC	383
	GTGCACCA**T**GGTGTCTG	384
Thalassaemia Beta TRP-16-Term TGG to TGA	TCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGT CTGCCGTTACTGCCCTGTG**G**GGCAAGGTGAACGTGGATGAA GTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTA	385
	TAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTC ATCCACGTTCACCTTGCC**C**CACAGGGCAGTAACGGCAGACT TCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA	386

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCCTGTG**G**GGCAAGGT	387
	ACCTTGCC**C**CACAGGGC	388
Thalassaemia Beta TRP-16-Term TGG to TAG	CTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTG**G**GGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTT	389
	AACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCATCCACGTTCACCTTGCCC**C**ACAGGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAG	390
	TGCCCTGT**G**GGGCAAGG	391
	CCTTGCCC**C**ACAGGGCA	392
Thalassaemia Beta LYS-18-Term AAG to TAG	ACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGC**A**AGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAG	393
	CTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCATCCACGTTCACCT**T**GCCCCACAGGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGT	394
	TGTGGGGC**A**AGGTGAAC	395
	GTTCACCT**T**GCCCCACA	396
Thalassaemia Beta ASN-20-SER AAC to AGC	CCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGA**A**CGTGGATGAAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTT	397
	AACCTGTCTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCATCCACG**T**TCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGG	398
	CAAGGTGA**A**CGTGGATG	399
	CATCCACG**T**TCACCTTG	400
Thalassaemia Beta GLU-23-ALA GAA to GCA	ACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATG**A**AGTTGGTGGTGAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGAC	401
	GTCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACT**T**CATCCACGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGT	402
	CGTGGATG**A**AGTTGGTG	403
	CACCAACT**T**CATCCACG	404

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta GLU-23-term GAA to TAA	CACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGTGAACGTGGAT**G**AAGTTGGTGGTGAGGCCCTG GGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA	405
	TCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCA GGGCCTCACCACCAACTT**C**ATCCACGTTCACCTTGCCCCACA GGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTG	406
	ACGTGGAT**G**AAGTTGGT	407
	ACCAACTT**C**ATCCACGT	408
Thalassaemia Beta GLU-27-LYS GAG to AAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGT**G**AGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAAACT	409
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCT**C**ACCACCAACTGCATCCACGTTCA CTTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	410
	TTGGTGGT**G**AGGCCCTG	411
	CAGGGCCT**C**ACCACCAA	412
Thalassaemia Beta GLU-27-Term GAG to TAG	GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGT**G**AGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAAACT	413
	AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCT**C**ACCACCAACTGCATCCACGTTCA CTTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC	414
	TTGGTGGT**G**AGGCCCTG	415
	CAGGGCCT**C**ACCACCAA	416
Thalassaemia Beta ALA-28-SER GCC to TCC	GAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAACGT GGATGCAGTTGGTGGTGAG**G**CCCTGGGCAGGTTGGTATCAA GGTTATAAGAGAGGCTCAAGGAGGCAAATGGAAACTGGG	417
	CCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGA TACCAACCTGCCCAGGG**C**CTCACCACCAACTGCATCCACGT TCACTTTGCCCCACAGGGCATTGACAGCAGTCTTCTC	418
	GTGGTGAG**G**CCCTGGGC	419
	GCCCAGGG**C**CTCACCAC	420

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta ARG-31-THR AGG to ACG	CTGTCAATGCCCTGTGGGGCAAAGTGAACGTGGATGCAGTT GGTGGTGAGGCCCTGGGCA**G**GTTGGTATCAAGGTTATAAGA GAGGCTCAAGGAGGCAAATGGAAACTGGGCATGTGTAGA	421
	TCTACACATGCCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTT ATAACCTTGATACCAAC**C**TGCCCAGGGCCTCACCACCAACTG CATCCACGTTCACTTTGCCCCACAGGGCATTGACAG	422
	CCTGGGCA**G**GTTGGTAT	423
	ATACCAAC**C**TGCCCAGG	424
Thalassaemia Beta Leu-33-GLN CTG to CAG	TGGGTTTCTGATAGGCACTGACTCTCTGTCCCTTGGGCTGTT TTCCTACCCTCAGATTAC**T**GGTGGTCTACCCTTGGACCCAGA GGTTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGA	425
	TCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAACCTCTG GGTCCAAGGGTAGACCACC**A**GTAATCTGAGGGTAGGAAAAC AGCCCAAGGGACAGAGAGTCAGTGCCTATCAGAAACCCA	426
	CAGATTAC**T**GGTGGTCT	427
	AGACCACC**A**GTAATCTG	428
Thalassaemia Beta TYR-36-Term TAC to TAA	ATAGGCACTGACTCTCTGTCCCTTGGGCTGTTTTCCTACCCT CAGATTACTGGTGGTCTA**C**CCTTGGACCCAGAGGTTCTTTGA GTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTATG	429
	CATAACAGCATCAGGAGAGGACAGATCCCCAAAGGACTCAAA GAACCTCTGGGTCCAAGG**G**TAGACCACCAGTAATCTGAGGG TAGGAAAACAGCCCAAGGGACAGAGAGTCAGTGCCTAT	430
	GTGGTCTA**C**CCTTGGAC	431
	GTCCAAGG**G**TAGACCAC	432
Thalassaemia Beta TRP-38-Term TGG to TGA	ACTGACTCTCTGTCCCTTGGGCTGTTTTCCTACCCTCAGATT ACTGGTGGTCTACCCTTG**G**ACCCAGAGGTTCTTTGAGTCCTT TGGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAAC	433
	GTTGCCCATAACAGCATCAGGAGAGGACAGATCCCCAAAGG ACTCAAAGAACCTCTGGGT**C**CAAGGGTAGACCACCAGTAATC TGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGT	434
	TACCCTTG**G**ACCCAGAG	435
	CTCTGGGT**C**CAAGGGTA	436
Thalassaemia Beta TRP-38-Term TGG to TAG	CACTGACTCTCTGTCCCTTGGGCTGTTTTCCTACCCTCAGAT TACTGGTGGTCTACCCTT**G**GACCCAGAGGTTCTTTGAGTCCT TTGGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAA	437

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGCCCATAACAGCATCAGGAGAGGACAGATCCCCAAAGGA CTCAAAGAACCTCTGGGTC**C**AAGGGTAGACCACCAGTAATCT GAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGTG	438
	CTACCCTT**G**GACCCAGA	439
	TCTGGGTC**C**AAGGGTAG	440
Thalassaemia Beta GLN-40-Term CAG-TAG	ACTCTCTGTCCCTTGGGCTGTTTTCCTACCCTCAGATTACTG GTGGTCTACCCTTGGACC**C**AGAGGTTCTTTGAGTCCTTTGGG GATCTGTCCTCTCCTGATGCTGTTATGGGCAACCCTA	441
	TAGGGTTGCCCATAACAGCATCAGGAGAGGACAGATCCCCA AAGGACTCAAAGAACCTCT**G**GGTCCAAGGGTAGACCACCAG TAATCTGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGT	442
	CTTGGACC**C**AGAGGTTC	443
	GAACCTCT**G**GGTCCAAG	444
Thalassaemia Beta GLU-44-Term GAG to TAG	TTGGGCTGTTTTCCTACCCTCAGATTACTGGTGGTCTACCCT TGGACCCAGAGGTTCTTT**G**AGTCCTTTGGGGATCTGTCCTCT CCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC	445
	GAGCCTTCACCTTAGGGTTGCCCATAACAGCATCAGGAGAG GACAGATCCCCAAAGGACT**C**AAAGAACCTCTGGGTCCAAGG GTAGACCACCAGTAATCTGAGGGTAGGAAAACAGCCCAA	446
	GGTTCTTT**G**AGTCCTTT	447
	AAAGGACT**C**AAAGAACC	448
Thalassaemia Beta LYS-62-Term AAG to TAG	TTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTA TGGGCAACCCTAAGGTG**A**AGGCTCATGGCAAGAAGGTGCTA GGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACC	449
	GGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGC ACCTTCTTGCCATGAGCCT**T**CACCTTAGGGTTGCCCATAACA GCATCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAA	450
	CTAAGGTG**A**AGGCTCAT	451
	ATGAGCCT**T**CACCTTAG	452
Thalassaemia Beta SER-73-ARG AGT to AGA	TGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGA AGGTGCTAGGTGCCTTTAG**T**GATGGCCTGGCTCACCTGGAC AACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCAC	453
	GTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTC CAGGTGAGCCAGGCCATC**A**CTAAAGGCACCTAGCACCTTCT TGCCATGAGCCTTCACCTTAGGGTTGCCCATAACAGCA	454

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCTTTAG**T**GATGGCCT	455
	AGGCCATC**A**CTAAAGGC	456
Haemolytic Anaemia GLY-75-VAL GGC to GTC	TTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTG CTAGGTGCCTTTAGTGATG**G**CCTGGCTCACCTGGACAACCT CAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCACTGTGA	457
	TCACAGTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAG GTTGTCCAGGTGAGCCAGG**C**CATCACTAAAGGCACCTAGCA CCTTCTTGCCATGAGCCTTCACCTTAGGGTTGCCCATAA	458
	TAGTGATG**G**CCTGGCTC	459
	GAGCCAGG**C**CATCACTA	460
Thalassaemia Beta GLU-91-Term GAG to TAG	GCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGG CACCTTTGCCACACTGAGT**G**AGCTGCACTGTGACAAGCTGC ACGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACC	461
	GGTCCCATAGACTCACCCTGAAGTTCTCAGGATCCACGTGCA GCTTGTCACAGTGCAGCT**C**ACTCAGTGTGGCAAAGGTGCCC TTGAGGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGC	462
	CACTGAGT**G**AGCTGCAC	463
	GTGCAGCT**C**ACTCAGTG	464
Thalassaemia Beta VAL-99-MET GTG to ATG	CTGGACAACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTG CACTGTGACAAGCTGCAC**G**TGGATCCTGAGAACTTCAGGGT GAGTCCAGGAGATGCTTCACTTTTCTCTTTTTACTTTC	465
	GAAAGTAAAAAGAGAAAAGTGAAGCATCTCCTGGACTCACCC TGAAGTTCTCAGGATCCA**C**GTGCAGCTTGTCACAGTGCAGCT CACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTCCAG	466
	AGCTGCAC**G**TGGATCCT	467
	AGGATCCA**C**GTGCAGCT	468
Thalassaemia Beta LEU-111-PRO CTG-CCG	CCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACA GCTCCTGGGCAACGTGC**T**GGTCTGTGTGCTGGCCCATCACT TTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTA	469
	TAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCCAAAGTG ATGGGCCAGCACACAGACC**A**GCACGTTGCCCAGGAGCTGTG GGAGGAAGATAAGAGGTATGAACATGATTAGCAAAAGGG	470
	CAACGTGC**T**GGTCTGTG	471
	CACAGACC**A**GCACGTTG	472

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia Beta CYS-113-Term TGT to TGA	GCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGCTCCTG GGCAACGTGCTGGTCTG**T**GTGCTGGCCCATCACTTTGGCAA AGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAA	473
	TTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCC AAAGTGATGGGCCAGCAC**A**CAGACCAGCACGTTGCCCAGGA GCTGTGGGAGGAAGATAAGAGGTATGAACATGATTAGC	474
	CTGGTCTG**T**GTGCTGGC	475
	GCCAGCAC**A**CAGACCAG	476
Thalassaemia Beta LEU-115-PRO CTG to CCG	TCATGTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCA ACGTGCTGGTCTGTGTGC**T**GGCCCATCACTTTGGCAAAGAAT TCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGT	477
	ACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCT TTGCCAAAGTGATGGGCC**A**GCACACAGACCAGCACGTTGCC CAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACATGA	478
	CTGTGTGC**T**GGCCCATC	479
	GATGGGCC**A**GCACACAG	480
Thalassaemia Beta ALA-116-ASP GCC to GAC	TGTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACG TGCTGGTCTGTGTGCTGG**C**CCATCACTTTGGCAAAGAATTCA CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGC	481
	GCCACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAA TTCTTTGCCAAAGTGATGG**G**CCAGCACACAGACCAGCACGTT GCCCAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACA	482
	TGTGCTGG**C**CCATCACT	483
	AGTGATGG**G**CCAGCACA	484
Thalassaemia Beta GLU-122-Term GAA to TAA	TTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCT GGCCCATCACTTTGGCAAA**G**AATTCACCCCACCAGTGCAGG CTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCC	485
	GGGCATTAGCCACACCAGCCACCACTTTCTGATAGGCAGCC TGCACTGGTGGGGTGAATT**C**TTTGCCAAAGTGATGGGCCAG CACACAGACCAGCACGTTGCCCAGGAGCTGTGGGAGGAA	486
	TTGGCAAA**G**AATTCACC	487
	GGTGAATT**C**TTTGCCAA	488
Thalassaemia Beta GLN-128-PRO CAG to CCG	GCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAA GAATTCACCCCACCAGTGC**A**GGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTA	489

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCAC CACTTTCTGATAGGCAGCC**T**GCACTGGTGGGGTGAATTCTTT GCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGC	490
	ACCAGTGC**A**GGCTGCCT	491
	AGGCAGCC**T**GCACTGGT	492
Thalassaemia Beta GLN-128-Term CAG to TAG	GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCCACCAGTG**C**AGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACT	493
	AGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCACC ACTTTCTGATAGGCAGCCT**G**CACTGGTGGGGTGAATTCTTTG CCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC	494
	CACCAGTG**C**AGGCTGCC	495
	GGCAGCCT**G**CACTGGTG	496
Thalassaemia Beta GLN-132-LYS CAG to AAG	GTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCA CCAGTGCAGGCTGCCTAT**C**AGAAAGTGGTGGCTGGTGTGGC TAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTC	497
	GAAAGCGAGCTTAGTGATACTTGTGGGCCAGGGCATTAGCC ACACCAGCCACCACTTTCT**G**ATAGGCAGCCTGCACTGGTGG GGTGAATTCTTTGCCAAAGTGATGGGCCAGCACACAGAC	498
	CTGCCTAT**C**AGAAAGTG	499
	CACTTTCT**G**ATAGGCAG	500

EXAMPLE 7
Retinoblastoma

Retinoblastoma (RB) is an embryonic neoplasm of retinal origin. It almost always presents in early childhood and is often bilateral. The risk of osteogenic sarcoma is increased 500-fold in bilateral retinoblastoma patients, the bone malignancy being at sites removed from those exposed to radiation treatment of the eye tumor.

The retinoblastoma susceptibility gene (pRB; pRb) plays a pivotal role in the regulation of the cell cycle. pRB restrains cell cycle progression by maintaining a checkpoint in late G_1 that controls commitment of cells to enter S phase. The critical role that pRB plays in cell cycle regulation explains its

status as archetypal tumor suppressor: loss of pRB function results in an inability to maintain control of the G_1 checkpoint; unchecked progression through the cell cycle is, in turn, a hallmark of neoplasia.

Blanquet *et al., Hum. Molec. Genet.* 4: 383-388 (1995) performed a mutation survey of the RB1 gene in 232 patients with hereditary or nonhereditary retinoblastoma. They systematically explored all 27 exons and flanking sequences, as well as the promoter. All types of point mutations were represented and found to be unequally distributed along the RB1 gene sequence. In the population studied, exons 3, 8, 18, and 19 were preferentially altered. The attached table discloses the correcting oligonucleotide base sequences for the retinoblastoma oligonucleotides of the invention.

Table 13
pRB Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Trp99Term TGG-TAG	AATATTTGATCTTTATTTTTTTGTTCCCAGGGAGGTTATATTCAA AAGAAAAAGGAACTGT**G**GGGAATCTGTATCTTTATTGCAGCA GTTGACCTAGATGAGATGTCGTTCACTTTTACTGA	501
	TCAGTAAAAGTGAACGACATCTCATCTAGGTCAACTGCTGCA ATAAAGATACAGATTCCC**C**ACAGTTCCTTTTTCTTTTGAATATA ACCTCCCTGGGAACAAAAAAATAAAGATCAAATATT	502
	GGAACTGT**G**GGGAATCT	503
	AGATTCCC**C**ACAGTTCC	504
Retinoblastoma Glu137Asp GAA-GAT	ATTTACTTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATTCTT TAACTTACTAAAAGA**A**ATTGATACCAGTACCAAAGTTGATAAT GCTATGTCAAGACTGTTGAAGAAGTATGATGTA	505
	TACATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTT TGGTACTGGTATCAAT**T**TCTTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAAGTAAAT	506
	CTAAAAGA**A**ATTGATAC	507
	GTATCAAT**T**TCTTTTAG	508
Retinoblastoma Glu137Term GAA-TAA	TGATTTACTTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATT CTTTAACTTACTAAAA**G**AAATTGATACCAGTACCAAAGTTGAT AATGCTATGTCAAGACTGTTGAAGAAGTATGATG	509

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTTT GGTACTGGTATCAATTT**C**TTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAAGTAAATCA	510
	TACTAAAA**G**AAATTGAT	511
	ATCAATTT**C**TTTTAGTA	512
Retinoblastoma Gln176Term CAA-TAA	AAAATGTTAAAAAGTCATAATGTTTTTCTTTTCAGGACATGTGA ACTTATATATTTGACA**C**AACCCAGCAGTTCGTAAGTAGTTCAC AGAATGTTATTTTTCACTTAAAAAAAAAGATTTT	513
	AAAATCTTTTTTTTTAAGTGAAAAATAACATTCTGTGAACTACT TACGAACTGCTGGGTT**G**TGTCAAATATATAAGTTCACATGTCC TGAAAAGAAAAACATTATGACTTTTTAACATTTT	514
	ATTTGACA**C**AACCCAGC	515
	GCTGGGTT**G**TGTCAAAT	516
Retinoblastoma Ile185Thr ATA-ACA	TGATACATTTTTCCTGTTTTTTTTCTGCTTTCTATTTGTTTAATA GGATATCTACTGAAA**T**AAATTCTGCATTGGTGCTAAAAGTTTC TTGGATCACATTTTTATTAGCTAAAGGTAAGTT	517
	AACTTACCTTTAGCTAATAAAAATGTGATCCAAGAAACTTTTA GCACCAATGCAGAATTT**A**TTTCAGTAGATATCCTATTAAACAA ATAGAAAGCAGAAAAAAAACAGGAAAAATGTATCA	518
	TACTGAAA**T**AAATTCTG	519
	CAGAATTT**A**TTTCAGTA	520
Retinoblastoma Gln207Term CAA-TAA	AAAGATCTGAATCTCTAACTTTCTTTAAAAATGTACATTTTTTT TTCAGGGGAAGTATTA**C**AAATGGAAGATGATCTGGTGATTTC ATTTCAGTTAATGCTATGTGTCCTTGACTATTTTA	521
	TAAAATAGTCAAGGACACATAGCATTAACTGAAATGAAATCAC CAGATCATCTTCCATTT**G**TAATACTTCCCCTGAAAAAAAAATG TACATTTTTAAAGAAAGTTAGAGATTCAGATCTTT	522
	AAGTATTA**C**AAATGGAA	523
	TTCCATTT**G**TAATACTT	524
Retinoblastoma Arg251Term CGA to TGA	GTTCTTATCTAATTTACCACTTTTACAGAAACAGCTGTTATACC CATTAATGGTTCACCT**C**GAACACCCAGGCGAGGTCAGAACA GGAGTGCACGGATAGCAAAACAACTAGAAAATGATA	525
	TATCATTTTCTAGTTGTTTTGCTATCCGTGCACTCCTGTTCTG ACCTCGCCTGGGTGTTC**G**AGGTGAACCATTAATGGGTATAAC AGCTGTTTCTGTAAAAGTGGTAAATTAGATAAGAAC	526

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTTCACCT**C**GAACACCC	527
	GGGTGTTC**G**AGGTGAAC	528
Retinoblastoma Arg255Term CGA to TGA	TTTACCACTTTTACAGAAACAGCTGTTATACCCATTAATGGTT CACCTCGAACACCCAGG**C**GAGGTCAGAACAGGAGTGCACG GATAGCAAAACAACTAGAAAATGATACAAGAATTATTG	529
	CAATAATTCTTGTATCATTTTCTAGTTGTTTTGCTATCCGTGCA CTCCTGTTCTGACCTC**G**CCTGGGTGTTCGAGGTGAACCATTA ATGGGTATAACAGCTGTTTCTGTAAAAGTGGTAAA	530
	CACCCAGG**C**GAGGTCAG	531
	CTGACCTC**G**CCTGGGTG	532
Retinoblastoma Gln266Term CAA to TAA	ATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAG GAGTGCACGGATAGCAAAA**C**AACTAGAAAATGATACAAGAAT TATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAG	533
	CTATATTACATTCATGTTCTTTACAGAGAACTTCAATAATTCTT GTATCATTTTCTAGTT**G**TTTTGCTATCCGTGCACTCCTGTTCT GACCTCGCCTGGGTGTTCGAGGTGAACCATTAAT	534
	TAGCAAAA**C**AACTAGAA	535
	TTCTAGTT**G**TTTTGCTA	536
Retinoblastoma Arg320Term CGA to TGA	TGACATGTAAAGGATAATTGTCAGTGACTTTTTTCTTTCAAGG TTGAAAATCTTTCTAAA**C**GATACGAAGAAATTTATCTTAAAAAT AAAGATCTAGATGCAAGATTATTTTTGGATCATG	537
	CATGATCCAAAAATAATCTTGCATCTAGATCTTTATTTTTAAGA TAAATTTCTTCGTATC**G**TTTAGAAAGATTTTCAACCTTGAAAGA AAAAAGTCACTGACAATTATCCTTTACATGTCA	538
	TTTCTAAA**C**GATACGAA	539
	TTCGTATC**G**TTTAGAAA	540
Retinoblastoma Gln354Term CAG to TAG	ACAAATTGTAAATTTTCAGTATGTGAATGACTTCACTTATTGTT ATTTAGTTTTGAAACA**C**AGAGAACACCACGAAAAAGTAACCTT GATGAAGAGGTGAATGTAATTCCTCCACACACTC	541
	GAGTGTGTGGAGGAATTACATTCACCTCTTCATCAAGGTTAC TTTTTCGTGGTGTTCTCT**G**TGTTTCAAAACTAAATAACAATAA GTGAAGTCATTCACATACTGAAAATTTACAATTTGT	542
	TTGAAACA**C**AGAGAACA	543
	TGTTCTCT**G**TGTTTCAA	544

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Arg358Gly CGA to GGA	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGAAACACAGAGAACACCA**C**GAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGTATG	545
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTTCATCAAGGTTACTTTTTC**G**TGGTGTTCTCTGTGTTTCAAAACTAAATAACAATAAGTGAAGTCATTCACATACTGAAAA	546
	GAACACCA**C**GAAAAAGT	547
	ACTTTTTC**G**TGGTGTTC	548
Retinoblastoma Arg358Term CGA to TGA	TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGAAACACAGAGAACACCA**C**GAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGTATG	549
	CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTTCATCAAGGTTACTTTTTC**G**TGGTGTTCTCTGTGTTTCAAAACTAAATAACAATAAGTGAAGTCATTCACATACTGAAAA	550
	GAACACCA**C**GAAAAAGT	551
	ACTTTTTC**G**TGGTGTTC	552
Retinoblastoma Ser397Term TCA to TAA	CTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATCAACCTT**C**AGAAAATCTGATTTCCTATTTTAACGTAAGCCATATATGAAACATTATTTATTGTAATAT	553
	ATATTACAATAAATAATGTTTCATATATGGCTTACGTTAAAATAGGAAATCAGATTTTCT**G**AAGGTTGATCACTTGCTGAATTTAAAATCATCATTAATTGTTGGATAGTGTTCATAACAG	554
	TCAACCTT**C**AGAAAATC	555
	GATTTTCT**G**AAGGTTGA	556
Retinoblastoma Arg445Term CGA to TGA	TTTCATAATTGTGATTTTCTAAAATAGCAGGCTCTTATTTTTCTTTTTGTTTGTTTGTAG**C**GATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGTAA	557
	TTACTGATTTAAGCATGGATTCCATTACTCGGTAATACAAGCGAACTCCAAGTTTGTATC**G**CTACAAACAAACAAAAAGAAAAATAAGAGCCTGCTATTTTAGAAAATCACAATTATGAAA	558
	GTTTGTAG**C**GATACAAA	559
	TTTGTATC**G**CTACAAAC	560
Retinoblastoma Arg455Term CGA to TGA	GCTCTTATTTTTCTTTTTGTTTGTTTGTAGCGATACAAACTTGGAGTTCGCTTGTATTAC**C**GAGTAATGGAATCCATGCTTAAATCAGTAAGTTAAAAACAATATAAAAAAATTTCAGCCG	561

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGGCTGAAATTTTTTTATATTGTTTTTAACTTACTGATTTAAGC ATGGATTCCATTACTC**G**GTAATACAAGCGAACTCCAAGTTTGT ATCGCTACAAACAAACAAAAAGAAAAATAAGAGC	562
	TGTATTAC**C**GAGTAATG	563
	CATTACTC**G**GTAATACA	564
Retinoblastoma Arg552Term CGA to TGA	ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAA ATGATAAAACATTTAGAA**C**GATGTGAACATCGAATCATGGAAT CCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTG	565
	CAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGATTCCAT GATTCGATGTTCACATC**G**TTCTAAATGTTTTATCATTTCTCTTG TCAAGTTGCCTTCTGCTTTGATAAAACTTTCGAT	566
	ATTTAGAA**C**GATGTGAA	567
	TTCACATC**G**TTCTAAAT	568
Retinoblastoma Cys553Term TGT to TGA	AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA AAACATTTAGAACGATG**T**GAACATCGAATCATGGAATCCCTTG CATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAA	569
	TTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGAT TCCATGATTCGATGTTC**A**CATCGTTCTAAATGTTTTATCATTTC TCTTGTCAAGTTGCCTTCTGCTTTGATAAAACTT	570
	GAACGATG**T**GAACATCG	571
	CGATGTTC**A**CATCGTTC	572
Retinoblastoma Glu554Term GAA to TAA	AGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAA AACATTTAGAACGATGT**G**AACATCGAATCATGGAATCCCTTG CATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAAA	573
	TTTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGA TTCCATGATTCGATGTT**C**ACATCGTTCTAAATGTTTTATCATTT CTCTTGTCAAGTTGCCTTCTGCTTTGATAAAACT	574
	AACGATGT**G**AACATCGA	575
	TCGATGTT**C**ACATCGTT	576
Retinoblastoma Ser567Leu TCA to TTA	TACCTGGGAAAATTATGCTTACTAATGTGGTTTTAATTTCATC ATGTTTCATATAGGATT**C**ACCTTTATTTGATCTTATTAAACAAT CAAAGGACCGAGAAGGACCAACTGATCACCTTGA	577
	TCAAGGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAA TAAGATCAAATAAAGGT**G**AATCCTATATGAAACATGATGAAAT TAAAACCACATTAGTAAGCATAATTTTCCCAGGTA	578

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAGGATT**C**ACCTTTAT	579
	ATAAAGGT**G**AATCCTAT	580
Retinoblastoma Gln575Term CAA to TAA	AATGTGGTTTTAATTTCATCATGTTTCATATAGGATTCACCTTT ATTTGATCTTATTAAA**C**AATCAAAGGACCGAGAAGGACCAACT GATCACCTTGAATCTGCTTGTCCTCTTAATCTTC	581
	GAAGATTAAGAGGACAAGCAGATTCAAGGTGATCAGTTGGTC CTTCTCGGTCCTTTGATT**G**TTTAATAAGATCAAATAAAGGTGA ATCCTATATGAAACATGATGAAATTAAAACCACATT	582
	TTATTAAA**C**AATCAAAG	583
	CTTTGATT**G**TTTAATAA	584
Retinoblastoma Arg579Term CGA to TGA	ATTTCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTAT TAAACAATCAAAGGAC**C**GAGAAGGACCAACTGATCACCTTGA ATCTGCTTGTCCTCTTAATCTTCCTCTCCAGAATA	585
	TATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAAGGT GATCAGTTGGTCCTTCTC**G**GTCCTTTGATTGTTTAATAAGATC AAATAAAGGTGAATCCTATATGAAACATGATGAAAT	586
	CAAAGGAC**C**GAGAAGGA	587
	TCCTTCTC**G**GTCCTTTG	588
Retinoblastoma Glu580Term GAA to TAA	TCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTATTAA ACAATCAAAGGACCGA**G**AAGGACCAACTGATCACCTTGAATC TGCTTGTCCTCTTAATCTTCCTCTCCAGAATAATC	589
	GATTATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAA GGTGATCAGTTGGTCCTT**C**TCGGTCCTTTGATTGTTTAATAAG ATCAAATAAAGGTGAATCCTATATGAAACATGATGA	590
	AGGACCGA**G**AAGGACCA	591
	TGGTCCTT**C**TCGGTCCT	592
Retinoblastoma Ser634Term TCA to TGA	AGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATG CAGAGACACAAGCAACCT**C**AGCCTTCCAGACCCAGAAGCCA TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGG	593
	CCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGGCT TCTGGGTCTGGAAGGCT**G**AGGTTGCTTGTGTCTCTGCATTTG CAGTAGAATTTACACGCGTAGTTGAACCTTTTTTCT	594
	AGCAACCT**C**AGCCTTCC	595
	GGAAGGCT**G**AGGTTGCT	596

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Ala635Pro GCC to CCC	AAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCA GAGACACAAGCAACCTCA**G**CCTTCCAGACCCAGAAGCCATT GAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGGTT	597
	AACCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGG CTTCTGGGTCTGGAAGG**C**TGAGGTTGCTTGTGTCTCTGCATT TGCAGTAGAATTTACACGCGTAGTTGAACCTTTTTT	598
	CAACCTCA**G**CCTTCCAG	599
	CTGGAAGG**C**TGAGGTTG	600
Retinoblastoma Gln639Term CAG to TAG	ACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCA ACCTCAGCCTTCCAGACC**C**AGAAGCCATTGAAATCTACCTCT CTTTCACTGTTTTATAAAAAAGGTTAGTAGATGATTA	601
	TAATCATCTACTAACCTTTTTTATAAAACAGTGAAAGAGAGGT AGATTTCAATGGCTTCT**G**GGTCTGGAAGGCTGAGGTTGCTTG TGTCTCTGCATTTGCAGTAGAATTTACACGCGTAGT	602
	TCCAGACC**C**AGAAGCCA	603
	TGGCTTCT**G**GGTCTGGA	604
Retinoblastoma Leu657Pro CTA to CCA	TTGTAATTCAAAATGAACAGTAAAAATGACTAATTTTTCTTATT CCCACAGTGTATCGGC**T**AGCCTATCTCCGGCTAAATACACTT TGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGA	605
	TCTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAAGTGTA TTTAGCCGGAGATAGGCT**A**GCCGATACACTGTGGGAATAAG AAAAATTAGTCATTTTTACTGTTCATTTTGAATTACAA	606
	GTATCGGC**T**AGCCTATC	607
	GATAGGCT**A**GCCGATAC	608
Retinoblastoma Arg661Trp CGG to TGG	AATGAACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTA TCGGCTAGCCTATCTC**C**GGCTAAATACACTTTGTGAACGCCT TCTGTCTGAGCACCCAGAATTAGAACATATCATCT	609
	AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGTATTTAGCC**G**GAGATAGGCTAGCCGATACACTG TGGGAATAAGAAAAATTAGTCATTTTTACTGTTCATT	610
	CCTATCTC**C**GGCTAAAT	611
	ATTTAGCC**G**GAGATAGG	612
Retinoblastoma Leu662Pro CTA to CCA	AACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTATCG GCTAGCCTATCTCCGGC**T**AAATACACTTTGTGAACGCCTTCT GTCTGAGCACCCAGAATTAGAACATATCATCTGGAC	613

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCCAGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGG CGTTCACAAAGTGTATTT**A**GCCGGAGATAGGCTAGCCGATAC ACTGTGGGAATAAGAAAAATTAGTCATTTTTACTGTT	614
	TCTCCGGC**T**AAATACAC	615
	GTGTATTT**A**GCCGGAGA	616
Retinoblastoma Glu675Term GAA to TAA	TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC CTTCTGTCTGAGCACCCA**G**AATTAGAACATATCATCTGGACC CTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCA	617
	TGAGTTCATACTCATTCTGCAGGGTGTGCTGGAAAAGGGTCC AGATGATATGTTCTAATT**C**TGGGTGCTCAGACAGAAGGCGTT CACAAAGTGTATTTAGCCGGAGATAGGCTAGCCGATA	618
	AGCACCCA**G**AATTAGAA	619
	TTCTAATT**C**TGGGTGCT	620
Retinoblastoma Gln685Pro CAG to CCG	TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA TCATCTGGACCCTTTTCC**A**GCACACCCTGCAGAATGAGTATG AACTCATGAGAGACAGGCATTTGGACCAAGTAAGAAA	621
	TTTCTTACTTGGTCCAAATGCCTGTCTCTCATGAGTTCATACT CATTCTGCAGGGTGTGC**T**GGAAAAGGGTCCAGATGATATGTT CTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAA	622
	CCTTTTCC**A**GCACACCC	623
	GGGTGTGC**T**GGAAAAGG	624
Retinoblastoma Cys706Tyr TGT to TAT	AAAACCATGTAATAAAATTCTGACTACTTTTACATCAATTTATT TACTAGATTATGATGT**G**TTCCATGTATGGCATATGCAAAGTGA AGAATATAGACCTTAAATTCAAAATCATTGTAAC	625
	GTTACAATGATTTTGAATTTAAGGTCTATATTCTTCACTTTGCA TATGCCATACATGGAA**C**ACATCATAATCTAGTAAATAAATTGA TGTAAAAGTAGTCAGAATTTTATTACATGGTTTT	626
	TATGATGT**G**TTCCATGT	627
	ACATGGAA**C**ACATCATA	628
Retinoblastoma Cys712Arg TGC to CGC	TTCTGACTACTTTTACATCAATTTATTTACTAGATTATGATGTG TTCCATGTATGGCATA**T**GCAAAGTGAAGAATATAGACCTTAAA TTCAAAATCATTGTAACAGCATACAAGGATCTTC	629
	GAAGATCCTTGTATGCTGTTACAATGATTTTGAATTTAAGGTC TATATTCTTCACTTTGC**A**TATGCCATACATGGAACACATCATA ATCTAGTAAATAAATTGATGTAAAAGTAGTCAGAA	630

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGGCATA**T**GCAAAGTG	631
	CACTTTGC**A**TATGCCAT	632
Retinoblastoma Tyr728Term TAC to TAA	GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAA ATCATTGTAACAGCATA**C**AAGGATCTTCCTCATGCTGTTCAG GAGGTAGGTAATTTTCCATAGTAAGTTTTTTTGATA	633
	TATCAAAAAAACTTACTATGGAAAATTACCTACCTCCTGAACA GCATGAGGAAGATCCTT**G**TATGCTGTTACAATGATTTTGAATT TAAGGTCTATATTCTTCACTTTGCATATGCCATAC	634
	ACAGCATA**C**AAGGATCT	635
	AGATCCTT**G**TATGCTGT	636
Retinoblastoma Glu748Term GAG to TAG	TTTTTTTTTTTTTTTTACTGTTCTTCCTCAGACATTCAAACGTGT TTTGATCAAAGAAGAG**G**AGTATGATTCTATTATAGTATTCTATA ACTCGGTCTTCATGCAGAGACTGAAAACAAATA	637
	TATTTGTTTTCAGTCTCTGCATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACT**C**CTCTTCTTTGATCAAAACACGTTTGA ATGTCTGAGGAAGAACAGTAAAAAAAAAAAAAAA	638
	AAGAAGAG**G**AGTATGAT	639
	ATCATACT**C**CTCTTCTT	640
Retinoblastoma Gln762Term CAG to TAG	GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCT ATAACTCGGTCTTCATG**C**AGAGACTGAAAACAAATATTTTGCA GTATGCTTCCACCAGGGTAGGTCAAAAGTATCCTT	641
	AAGGATACTTTTGACCTACCCTGGTGGAAGCATACTGCAAAA TATTTGTTTTCAGTCTCT**G**CATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACTCCTCTTCTTTGATCAAAAC	642
	TCTTCATG**C**AGAGACTG	643
	CAGTCTCT**G**CATGAAGA	644
Retinoblastoma Arg787Term CGA-TGA	TAATCTACTTTTTTGTTTTTGCTCTAGCCCCCTACCTTGTCAC CAATACCTCACATTCCT**C**GAAGCCCTTACAAGTTTCCTAGTTC ACCCTTACGGATTCCTGGAGGGAACATCTATATTT	645
	AAATATAGATGTTCCCTCCAGGAATCCGTAAGGGTGAACTAG GAAACTTGTAAGGGCTTC**G**AGGAATGTGAGGTATTGGTGACA AGGTAGGGGGCTAGAGCAAAAACAAAAAAGTAGATTA	646
	ACATTCCT**C**GAAGCCCT	647
	AGGGCTTC**G**AGGAATGT	648

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Retinoblastoma Ser816Term TCA to TGA	CCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGA AGAGTCCATATAAAATTT**C**AGAAGGTCTGCCAACACCAACAA AAATGACTCCAAGATCAAGGTGTGTGTTTTCTCTTTA	649
	TAAAGAGAAAACACACACCTTGATCTTGGAGTCATTTTTGTTG GTGTTGGCAGACCTTCT**G**AAATTTTATATGGACTCTTCAGGG GTGAAATATAGATGTTCCCTCCAGGAATCCGTAAGG	650
	TAAAATTT**C**AGAAGGTC	651
	GACCTTCT**G**AAATTTTA	652

EXAMPLE 8
BRCA1 and BRCA2

Breast cancer is the second major cause of cancer death in American women, with an estimated 44,190 lives lost (290 men and 43,900 women) in the US in 1997. While ovarian cancer accounts for fewer deaths than breast cancer, it still represents 4% of all female cancers. In 1994, two breast cancer susceptibility genes were identified: BRCA1 on chromosome 17 and BRCA2 on chromosome 13. When a woman carries a mutation in either BRCA1 or BRCA2, she is at increased risk of being diagnosed with breast or ovarian cancer at some point in her life.

Ford *et al., Am. J. Hum. Genet.* 62: 676-689 (1998) assessed the contribution of BRCA1 and BRCA2 to inherited breast cancer by linkage and mutation analysis in 237 families, each with at least 4 cases of breast cancer. Families were included without regard to the occurrence of ovarian or other cancers. Overall, disease was linked to BRCA1 in an estimated 52% of families, to BRCA2 in 32% of families, and to neither gene in 16%, suggesting other predisposition genes. The majority (81%) of the breast-ovarian cancer families were due to BRCA1, with most others (14%) due to BRCA2. Conversely, the majority (76%) of families with both male and female breast cancer were due to BRCA2. The largest proportion (67%) of families due to other genes were families with 4 or 5 cases of female breast cancer only.

More than 75% of the reported mutations in the BRCA1 gene result in truncated proteins. Couch *et al., Hum. Mutat.* 8: 8-18, 1996. (1996) reported a total of 254 BRCA1 mutations, 132 (52%) of which were unique. A total of 221 (87%) of all mutations or 107 (81%) of the unique mutations are small deletions, insertions, nonsense point mutations, splice variants, and regulatory mutations that result in

truncation or absence of the BRCA1 protein. A total of 11 disease-associated missense mutations (5 unique) and 21 variants (19 unique) as yet unclassified as missense mutations or polymorphisms had been detected. Thirty-five independent benign polymorphisms had been described. The most common mutations were 185delAG and 5382insC, which accounted for 30 (11.7%) and 26 (10.1%), respectively, of all the mutations.

Most BRCA2 mutations are predicted to result in a truncated protein product. The smallest known cancer-associated deletion removes from the C terminus only 224 of the 3,418 residues constituting BRCA2, suggesting that these terminal amino acids are critical for BRCA2 function. Studies (Spain *et al.*, Proc. Natl. Acad. Sci. 96:13920-13925 (1999)) suggest that such truncations eliminate or interfere with 2 nuclear localization signals that reside within the final 156 residues of BRCA2, suggesting that the vast majority of BRCA2 mutants are nonfunctional because they are not translocated into the nucleus.

The attached table discloses the correcting oligonucleotide base sequences for the BRACA1 and BRACA2 oligonucleotides of the invention.

Table 14
BRCA1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Met-1-Ile ATG to ATT	CTGCGCTCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGTT CATTGGAACAGAAAGAAATGGATTTATCTGCTCTTCGCGTTG AAGAAGTACAAAATGTCATTAATGCTATGCAGAAAATC	653
	GATTTTCTGCATAGCATTAATGACATTTTGTACTTCTTCAACG CGAAGAGCAGATAAATCCATTTCTTTCTGTTCCAATGAACTTT ACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAG	654
	AAAGAAATGGATTTATC	655
	GATAAATCCATTTCTTT	656
Breast Cancer Val-11-Ala GTA to GCA	CTGGGTAAAGTTCATTGGAACAGAAAGAAATGGATTTATCTG CTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGCA GAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGAT	657
	ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCTGCATA GCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATA AATCCATTTCTTTCTGTTCCAATGAACTTTACCCAG	658
	TGAAGAAGTACAAAATG	659

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATTTTGTACTTCTTCA	660
Breast Cancer Ile-21-Val ATC to GTC	ATGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCA TTAATGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGG AGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	661
	GGTCACACTTTGTGGAGACAGGTTCCTTGATCAACTCCAGAC AGATGGGACACTCTAAGATTTTCTGCATAGCATTAATGACATT TTGTACTTCTTCAACGCGAAGAGCAGATAAATCCAT	662
	TGCAGAAAATCTTAGAG	663
	CTCTAAGATTTTCTGCA	664
Breast Cancer Leu-22-Ser TTA to TCA	ATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAA TGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTT GATCAAGGAACCTGTCTCCACAAAGTGTGACCACAT	665
	ATGTGGTCACACTTTGTGGAGACAGGTTCCTTGATCAACTCC AGACAGATGGGACACTCTAAGATTTTCTGCATAGCATTAATG ACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAAT	666
	GAAAATCTTAGAGTGTC	667
	GACACTCTAAGATTTTC	668
Breast Cancer Cys-39-Tyr TGT to TAT	AGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGG AACCTGTCTCCACAAAGTGTGACCACATATTTTGCAAATTTTG CATGCTGAAACTTCTCAACCAGAAGAAAGGGCCTTC	669
	GAAGGCCCTTTCTTCTGGTTGAGAAGTTTCAGCATGCAAAAT TTGCAAAATATGTGGTCACACTTTGTGGAGACAGGTTCCTTG ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCT	670
	CACAAAGTGTGACCACA	671
	TGTGGTCACACTTTGTG	672
Breast Cancer Cys-61-Gly TGT to GGT	CACATATTTTGCAAATTTTGCATGCTGAAACTTCTCAACCAGA AGAAAGGGCCTTCACAGTGTCCTTTATGTAAGAATGATATAAC CAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC	673
	GACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATC ATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTCTGGTT GAGAAGTTTCAGCATGCAAAATTTGCAAAATATGTG	674
	CTTCACAGTGTCCTTTA	675
	TAAAGGACACTGTGAAG	676

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Leu-63-Stop TTA to TAA	TTTGCAAATTTTGCATGCTGAAACTTCTCAACCAGAAGAAAGG GCCTTCACAGTGTCCTT**T**ATGTAAGAATGATATAACCAAAAGG AGCCTACAAGAAAGTACGAGATTTAGTCAACTTGT	677
	ACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGG TTATATCATTCTTACAT**A**AAGGACACTGTGAAGGCCCTTTCTT CTGGTTGAGAAGTTTCAGCATGCAAAATTTGCAAA	678
	GTGTCCTT**T**ATGTAAGA	679
	TCTTACAT**A**AAGGACAC	680
Breast Cancer Cys-64-Arg TGT to CGT Breast Cancer Cys-64-Gly TGT to GGT	TGCAAATTTTGCATGCTGAAACTTCTCAACCAGAAGAAAGGG CCTTCACAGTGTCCTTTA**T**GTAAGAATGATATAACCAAAAGGA GCCTACAAGAAAGTACGAGATTTAGTCAACTTGTTG	681
	CAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTT GGTTATATCATTCTTAC**A**TAAAGGACACTGTGAAGGCCCTTTC TTCTGGTTGAGAAGTTTCAGCATGCAAAATTTGCA	682
	GTCCTTTA**T**GTAAGAAT	683
	ATTCTTAC**A**TAAAGGAC	684
Breast Cancer Cys-64-Tyr TGT to TAT	GCAAATTTTGCATGCTGAAACTTCTCAACCAGAAGAAAGGGC CTTCACAGTGTCCTTTAT**G**TAAGAATGATATAACCAAAAGGAG CCTACAAGAAAGTACGAGATTTAGTCAACTTGTTGA	685
	TCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTT TGGTTATATCATTCTTA**C**ATAAAGGACACTGTGAAGGCCCTTT CTTCTGGTTGAGAAGTTTCAGCATGCAAAATTTGC	686
	TCCTTTAT**G**TAAGAATG	687
	CATTCTTA**C**ATAAAGGA	688
Breast Cancer Gln-74-Stop CAA to TAA	CAGAAGAAAGGGCCTTCACAGTGTCCTTTATGTAAGAATGAT ATAACCAAAAGGAGCCTA**C**AAGAAAGTACGAGATTTAGTCAA CTTGTTGAAGAGCTATTGAAAATCATTTGTGCTTTTC	689
	GAAAAGCACAAATGATTTTCAATAGCTCTTCAACAAGTTGACT AAATCTCGTACTTTCTT**G**TAGGCTCCTTTTGGTTATATCATTCT TACATAAAGGACACTGTGAAGGCCCTTTCTTCTG	690
	GGAGCCTA**C**AAGAAAGT	691
	ACTTTCTT**G**TAGGCTCC	692

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Tyr-105-Cys TAT to TGT	AGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTT GGAGTATGCAAACAGCT**A**TAATTTTGCAAAAAAGGAAAATAAC TCTCCTGAACATCTAAAAGATGAAGTTTCTATCAT	693
	ATGATAGAAACTTCATCTTTTAGATGTTCAGGAGAGTTATTTT CCTTTTTTGCAAAATTA**T**AGCTGTTTGCATACTCCAAACCTGT GTCAAGCTGAAAAGCACAAATGATTTTCAATAGCT	694
	AAACAGCT**A**TAATTTTG	695
	CAAAATTA**T**AGCTGTTT	696
Breast Cancer Asn-158-Tyr AAC to TAC	CTACAGAGTGAACCCGAAAATCCTTCCTTGCAGGAAACCAGT CTCAGTGTCCAACTCTCT**A**ACCTTGGAACTGTGAGAACTCTG AGGACAAAGCAGCGGATACAACCTCAAAAGACGTCTG	697
	CAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAG TTCTCACAGTTCCAAGGT**T**AGAGAGTTGGACACTGAGACTGG TTTCCTGCAAGGAAGGATTTTCGGGTTCACTCTGTAG	698
	AACTCTCT**A**ACCTTGGA	699
	TCCAAGGT**T**AGAGAGTT	700
Breast Cancer Gln-169-Stop CAG to TAG	GAAACCAGTCTCAGTGTCCAACTCTCTAACCTTGGAACTGTG AGAACTCTGAGGACAAAG**C**AGCGGATACAACCTCAAAAGAC GTCTGTCTACATTGAATTGGGATCTGATTCTTCTGAAG	701
	CTTCAGAAGAATCAGATCCCAATTCAATGTAGACAGACGTCTT TTGAGGTTGTATCCGCT**G**CTTTGTCCTCAGAGTTCTCACAGT TCCAAGGTTAGAGAGTTGGACACTGAGACTGGTTTC	702
	GGACAAAG**C**AGCGGATA	703
	TATCCGCT**G**CTTTGTCC	704
Breast Cancer Trp-353-Stop TGG to TAG	CTCCCAGCACAGAAAAAAAGGTAGATCTGAATGCTGATCCCC TGTGTGAGAGAAAAGAAT**G**GAATAAGCAGAAACTGCCATGCT CAGAGAATCCTAGAGATACTGAAGATGTTCCTTGGAT	705
	ATCCAAGGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT GGCAGTTTCTGCTTATTC**C**ATTCTTTTCTCTCACACAGGGGAT CAGCATTCAGATCTACCTTTTTTTCTGTGCTGGGAG	706
	AAAAGAAT**G**GAATAAGC	707
	GCTTATTC**C**ATTCTTTT	708
Breast Cancer Ile-379-Met ATT to ATG	ATGCTCAGAGAATCCTAGAGATACTGAAGATGTTCCTTGGAT AACACTAAATAGCAGCAT**T**CAGAAAGTTAATGAGTGGTTTTCC AGAAGTGATGAACTGTTAGGTTCTGATGACTCACAT	709

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGGAAAAC CACTCATTAACTTTCTGAATGCTGCTATTTAGTGTTATCCAAG GAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT	710
	AGCAGCATTCAGAAAGT	711
	ACTTTCTGAATGCTGCT	712
Breast Cancer Glu-421-Gly GAA to GGA	GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTATTGGACG TTCTAAATGAGGTAGATGAATATTCTGGTTCTTCAGAGAAAAT AGACTTACTGGCCAGTGATCCTCATGAGGCTTTAAT	713
	ATTAAAGCCTCATGAGGATCACTGGCCAGTAAGTCTATTTTCT CTGAAGAACCAGAATATTCATCTACCTCATTTAGAACGTCCAA TACATCAGCTACTTTGGCATTTGATTCAGACTCCC	714
	GGTAGATGAATATTCTG	715
	CAGAATATTCATCTACC	716
Breast Cancer Phe-461-Leu TTT to CTT	ATATGTAAAAGTGAAAGAGTTCACTCCAAATCAGTAGAGAGTA ATATTGAAGACAAAATATTTGGGAAAACCTATCGGAAGAAGG CAAGCCTCCCCAACTTAAGCCATGTAACTGAAAATC	717
	GATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCT TCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACTCTCT ACTGATTTGGAGTGAACTCTTTCACTTTTACATAT	718
	ACAAAATATTTGGGAAA	719
	TTTCCCAAATATTTTGT	720
Breast Cancer Tyr-465-Leu TAT to GAT	GAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGAC AAAATATTTGGGAAAACCTATCGGAAGAAGGCAAGCCTCCCC AACTTAAGCCATGTAACTGAAAATCTAATTATAGGAG	721
	CTCCTATAATTAGATTTTCAGTTACATGGCTTAAGTTGGGGAG GCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCA ATATTACTCTCTACTGATTTGGAGTGAACTCTTTC	722
	GGAAAACCTATCGGAAG	723
	CTTCCGATAGGTTTTCC	724
Breast Cancer Gly-484-Stop GGA to TGA	ACCTATCGGAAGAAGGCAAGCCTCCCCAACTTAAGCCATGTA ACTGAAAATCTAATTATAGGAGCATTTGTTACTGAGCCACAGA TAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC	725
	GCTTTAATTTATTTGTGAGGGGACGCTCTTGTATTATCTGTGG CTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG CTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGT	726

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATTATA**G**GAGCATTT	727
	AAATGCTC**C**TATAATTA	728
Breast Cancer Arg-507-Ile AGA to ATA	TTACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATA AATTAAAGCGTAAAAGGA**G**ACCTACATCAGGCCTTCATCCTG AGGATTTTATCAAGAAAGCAGATTTGGCAGTTCAAAA	729
	TTTTGAACTGCCAAATCTGCTTTCTTGATAAAATCCTCAGGAT GAAGGCCTGATGTAGGT**C**TCCTTTTACGCTTTAATTTATTTGT GAGGGGACGCTCTTGTATTATCTGTGGCTCAGTAA	730
	TAAAAGGA**G**ACCTACAT	731
	ATGTAGGT**C**TCCTTTTA	732
Breast Cancer Ser-510-Stop TCA to TGA	CACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC GTAAAAGGAGACCTACAT**C**AGGCCTTCATCCTGAGGATTTTA TCAAGAAAGCAGATTTGGCAGTTCAAAAGACTCCTGA	733
	TCAGGAGTCTTTTGAACTGCCAAATCTGCTTTCTTGATAAAAT CCTCAGGATGAAGGCCT**G**ATGTAGGTCTCCTTTTACGCTTTA ATTTATTTGTGAGGGGACGCTCTTGTATTATCTGTG	734
	ACCTACAT**C**AGGCCTTC	735
	GAAGGCCT**G**ATGTAGGT	736
Breast Cancer Gln-526-Stop CAA to TAA	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTT**C**AAAAGACTCCTGAAATGATAAATC AGGGAACTAACCAAACGGAGCAGAATGGTCAAGTGA	737
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT**G**AACTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	738
	TGGCAGTT**C**AAAAGACT	739
	AGTCTTTT**G**AACTGCCA	740
Breast Cancer Gln-541-Stop CAG to TAG	AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTT**C**AAAAGACTCCTGAAATGATAAATC AGGGAACTAACCAAACGGAGCAGAATGGTCAAGTGA	741
	TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT**G**AACTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT	742
	AAACGGAG**C**AGAATGGT	743
	ACCATTCT**G**CTCCGTTT	744

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Gly-552-Val GGT to GTT	TAAATCAGGGAACTAACCAAACGGAGCAGAATGGTCAAGTGA TGAATATTACTAATAGTGGTCATGAGAATAAAACAAAAGGTGA TTCTATTCAGAATGAGAAAAATCCTAACCCAATAGA	745
	TCTATTGGGTTAGGATTTTTCTCATTCTGAATAGAATCACCTTT TGTTTTATTCTCATGACCACTATTAGTAATATTCATCACTTGAC CATTCTGCTCCGTTTGGTTAGTTCCCTGATTTA	746
	TAATAGTGGTCATGAGA	747
	TCTCATGACCACTATTA	748
Breast Cancer Gln-563-Stop CAG to TAG	GGTCAAGTGATGAATATTACTAATAGTGGTCATGAGAATAAAA CAAAAGGTGATTCTATTCAGAATGAGAAAAATCCTAACCCAAT AGAATCACTCGAAAAAGAATCTGCTTTCAAAACGA	749
	TCGTTTTGAAAGCAGATTCTTTTTCGAGTGATTCTATTGGGTT AGGATTTTTCTCATTCTGAATAGAATCACCTTTTGTTTTATTCT CATGACCACTATTAGTAATATTCATCACTTGACC	750
	ATTCTATTCAGAATGAG	751
	CTCATTCTGAATAGAAT	752
Ovarian Cancer Lys-607-Stop AAA to TAA	ATAAGCAGCAGTATAAGCAATATGGAACTCGAATTAAATATCC ACAATTCAAAAGCACCTAAAAAGAATAGGCTGAGGAGGAAGT CTTCTACCAGGCATATTCATGCGCTTGAACTAGTAG	753
	CTACTAGTTCAAGCGCATGAATATGCCTGGTAGAAGACTTCC TCCTCAGCCTATTCTTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTAT	754
	AAGCACCTAAAAAGAAT	755
	ATTCTTTTTAGGTGCTT	756
Breast Cancer Leu-639-Stop TTG to TAG	ATATTCATGCGCTTGAACTAGTAGTCAGTAGAAATCTAAGCCC ACCTAATTGTACTGAATTGCAAATTGATAGTTGTTCTAGCAGT GAAGAGATAAAGAAAAAAAAGTACAACCAAATGCC	757
	GGCATTTGGTTGTACTTTTTTTTCTTTATCTCTTCACTGCTAGA ACAACTATCAATTTGCAATTCAGTACAATTAGGTGGGCTTAGA TTTCTACTGACTACTAGTTCAAGCGCATGAATAT	758
	TACTGAATTGCAAATTG	759
	CAATTTGCAATTCAGTA	760
Breast Cancer Asp-693-Asn GAC to AAC	GAACCTGCAACTGGAGCCAAGAAGAGTAACAAGCCAAATGAA CAGACAAGTAAAAGACATGACAGCGATACTTTCCCAGAGCTG AAGTTAACAAATGCACCTGGTTCTTTTACTAAGTGTT	761

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AACACTTAGTAAAAGAACCAGGTGCATTTGTTAACTTCAGCTC TGGGAAAGTATCGCTGT**C**ATGTCTTTTACTTGTCTGTTCATTT GGCTTGTTACTCTTCTTGGCTCCAGTTGCAGGTTC	762
	AAAGACAT**G**ACAGCGAT	763
	ATCGCTGT**C**ATGTCTTT	764
Ovarian Cancer Glu-720-Stop GAA to TAA	CTGAAGTTAACAAATGCACCTGGTTCTTTTACTAAGTGTTCAA ATACCAGTGAACTTAAA**G**AATTTGTCAATCCTAGCCTTCCAAG AGAAGAAAAAGAAGAGAAACTAGAAACAGTTAAAG	765
	CTTTAACTGTTTCTAGTTTCTCTTCTTTTTCTTCTCTTGGAAGG CTAGGATTGACAAATT**C**TTTAAGTTCACTGGTATTTGAACACT TAGTAAAAGAACCAGGTGCATTTGTTAACTTCAG	766
	AACTTAAA**G**AATTTGTC	767
	GACAAATT**C**TTTAAGTT	768
Breast Cancer Glu-755-Stop GAA to TAA	CTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAA GATCTCATGTTAAGTGGA**G**AAAGGGTTTTGCAAACTGAAAGA TCTGTAGAGAGTAGCAGTATTTCATTGGTACCTGGTA	769
	TACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTC AGTTTGCAAAACCCTTT**C**TCCACTTAACATGAGATCTTTGGGG TCTTCAGCATTATTAGACACTTTAACTGTTTCTAG	770
	TAAGTGGA**G**AAAGGGTT	771
	AACCCTTT**C**TCCACTTA	772
Breast Cancer Ser-770-Stop TCA to TAA	TCATGTTAAGTGGAGAAAGGGTTTTGCAAACTGAAAGATCTG TAGAGAGTAGCAGTATTT**C**ATTGGTACCTGGTACTGATTATG GCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAC	773
	GTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAA TCAGTACCAGGTACCAAT**G**AAATACTGCTACTCTCTACAGAT CTTTCAGTTTGCAAAACCCTTTCTCCACTTAACATGA	774
	CAGTATTT**C**ATTGGTAC	775
	GTACCAAT**G**AAATACTG	776
Breast Cancer Val-772-Ala GTA to GCA	TAAGTGGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGA GTAGCAGTATTTCATTGG**T**ACCTGGTACTGATTATGGCACTC AGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGG	777
	CCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTG CCATAATCAGTACCAGGT**A**CCAATGAAATACTGCTACTCTCTA CAGATCTTTCAGTTTGCAAAACCCTTTCTCCACTTA	778

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCATTGG**T**ACCTGGTA	779
	TACCAGGT**A**CCAATGAA	780
Breast Cancer Gln-780-Stop CAG to TAG	ACTGAAAGATCTGTAGAGAGTAGCAGTATTTCATTGGTACCT GGTACTGATTATGGCACT**C**AGGAAAGTATCTCGTTACTGGAA GTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATA	781
	TATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAG TAACGAGATACTTTCCT**G**AGTGCCATAATCAGTACCAGGTAC CAATGAAATACTGCTACTCTCTACAGATCTTTCAGT	782
	ATGGCACT**C**AGGAAAGT	783
	ACTTTCCT**G**AGTGCCAT	784
Breast Cancer Glu-797-Stop GAA to TAA	TATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACT CTAGGGAAGGCAAAAACA**G**AACCAAATAAATGTGTGAGTCAG TGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATG	785
	CATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGAC TCACACATTTATTTGGTT**C**TGTTTTTGCCTTCCCTAGAGTGCT AACTTCCAGTAACGAGATACTTTCCTGAGTGCCATA	786
	CAAAAACA**G**AACCAAAT	787
	ATTTGGTT**C**TGTTTTTG	788
Breast Cancer Lys-820-Glu AAA to GAA	AAATGTGTGAGTCAGTGTGCAGCATTTGAAAACCCCAAGGGA CTAATTCATGGTTGTTCC**A**AAGATAATAGAAATGACACAGAAG GCTTTAAGTATCCATTGGGACATGAAGTTAACCACA	789
	TGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGT GTCATTTCTATTATCTT**T**GGAACAACCATGAATTAGTCCCTTG GGGTTTTCAAATGCTGCACACTGACTCACACATTT	790
	GTTGTTCC**A**AAGATAAT	791
	ATTATCTT**T**GGAACAAC	792
Breast Cancer Thr-826-Lys ACA to AAA	CAGCATTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCA AAGATAATAGAAATGACA**C**AGAAGGCTTTAAGTATCCATTGG GACATGAAGTTAACCACAGTCGGGAAACAAGCATAGA	793
	TCTATGCTTGTTTCCCGACTGTGGTTAACTTCATGTCCCAATG GATACTTAAAGCCTTCT**G**TGTCATTTCTATTATCTTTGGAACA ACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTG	794
	AAATGACA**C**AGAAGGCT	795
	AGCCTTCT**G**TGTCATTT	796

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Arg-841-Trp CGG to TGG	GATAATAGAAATGACACAGAAGGCTTTAAGTATCCATTGGGA CATGAAGTTAACCACAGT**C**GGGAAACAAGCATAGAAATGGAA GAAAGTGAACTTGATGCTCAGTATTTGCAGAATACAT	797
	ATGTATTCTGCAAATACTGAGCATCAAGTTCACTTTCTTCCAT TTCTATGCTTGTTTCCC**G**ACTGTGGTTAACTTCATGTCCCAAT GGATACTTAAAGCCTTCTGTGTCATTTCTATTATC	798
	ACCACAGT**C**GGGAAACA	799
	TGTTTCCC**G**ACTGTGGT	800
Breast Cancer Pro-871-Leu CCG to CTG	AACTTGATGCTCAGTATTTGCAGAATACATTCAAGGTTTCAAA GCGCCAGTCATTTGCTC**C**GTTTTCAAATCCAGGAAATGCAGA AGAGGAATGTGCAACATTCTCTGCCCACTCTGGGTC	801
	GACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCA TTTCCTGGATTTGAAAAC**G**GAGCAAATGACTGGCGCTTTGAA ACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTT	802
	ATTTGCTC**C**GTTTTCAA	803
	TTGAAAAC**G**GAGCAAAT	804
Breast Cancer Leu-892-Ser TTA to TCA	TTTCAAATCCAGGAAATGCAGAAGAGGAATGTGCAACATTCT CTGCCCACTCTGGGTCCT**T**AAAGAAACAAAGTCCAAAAGTCA CTTTTGAATGTGAACAAAAGGAAGAAAATCAAGGAAA	805
	TTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGACTTT TGGACTTTGTTTCTTT**A**AGGACCCAGAGTGGGCAGAGAATGT TGCACATTCCTCTTCTGCATTTCCTGGATTTGAAA	806
	TGGGTCCT**T**AAAGAAAC	807
	GTTTCTTT**A**AGGACCCA	808
Breast Cancer Glu-908-Stop GAA to TAA	CACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTTTTG AATGTGAACAAAAGGAA**G**AAAATCAAGGAAAGAATGAGTCTA ATATCAAGCCTGTACAGACAGTTAATATCACTGCAG	809
	CTGCAGTGATATTAACTGTCTGTACAGGCTTGATATTAGACTC ATTCTTTCCTTGATTTT**C**TTCCTTTTGTTCACATTCAAAAGTGA CTTTTGGACTTTGTTTCTTTAAGGACCCAGAGTG	810
	AAAAGGAA**G**AAAATCAA	811
	TTGATTTT**C**TTCCTTTT	812
Breast Cancer Gly-960-Asp GGC to GAC	ATAATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTCT ATCATCTCAGTTCAGAG**G**CAACGAAACTGGACTCATTACTCC AAATAAACATGGACTTTTACAAAACCCATATCGTAT	813

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATACGATATGGGTTTTGTAAAAGTCCATGTTTATTTGGAGTAA TGAGTCCAGTTTCGTTG**C**CTCTGAACTGAGATGATAGACAAA ACCTAGAGCCTCCTTTGATACTACATTTGGCATTAT	814
	GTTCAGAG**G**CAACGAAA	815
	TTTCGTTG**C**CTCTGAAC	816
Breast Cancer Met-1008-Ile ATG to ATA	ATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGGAAAAC TTTGAGGAACATTCAATG**G**TCACCTGAAAGAGAAATGGGAAAT GAGAACATTCCAAGTACAGTGAGCACAATTAGCCGT	817
	ACGGCTAATTGTGCTCACTGTACTTGGAATGTTCTCATTTCCC ATTTCTCTTTCAGGTGA**C**ATTGAATGTTCCTCAAAGTTTTCCT CTAGCAGATTTTTCTTACATTTAGTTTTAACAAAT	818
	CATTCAAT**G**TCACCTGA	819
	TCAGGTGA**C**ATTGAATG	820
Breast Cancer Thr-1025-Ile ACA to ATA	ACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAA ATGAGAACATTCCAAGTA**C**AGTGAGCACAATTAGCCGTAATA ACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTCAAG	821
	CTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTATTACG GCTAATTGTGCTCACT**G**TACTTGGAATGTTCTCATTTCCCATT TCTCTTTCAGGTGACATTGAATGTTCCTCAAAGT	822
	TCCAAGTA**C**AGTGAGCA	823
	TGCTCACT**G**TACTTGGA	824
Breast Cancer Glu-1038-Gly GAA to GGA	ACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAG AGAAAATGTTTTTAAAG**A**AGCCAGCTCAAGCAATATTAATGAA GTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTAT	825
	ATACTGGAGCCCACTTCATTAGTACTGGAACCTACTTCATTAA TATTGCTTGAGCTGGCT**T**CTTTAAAAACATTTTCTCTAATGTTA TTACGGCTAATTGTGCTCACTGTACTTGGAATGT	826
	TTTTAAAG**A**AGCCAGCT	827
	AGCTGGCT**T**CTTTAAAA	828
Breast Cancer Ser-1040-Asn AGC to AAC	CAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAA ATGTTTTTAAAGAAGCCA**G**CTCAAGCAATATTAATGAAGTAGG TTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	829
	TCATTAATACTGGAGCCCACTTCATTAGTACTGGAACCTACTT CATTAATATTGCTTGAG**C**TGGCTTCTTTAAAAACATTTTCTCTA ATGTTATTACGGCTAATTGTGCTCACTGTACTTG	830

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAAGCCAGCTCAAGCA	831
	TGCTTGAGCTGGCTTCT	832
Breast Cancer Val-1047-Ala GTA to GCA	GCCGTAATAACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTC AAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGG CTCCAGTATTAATGAAATAGGTTCCAGTGATGAAAA	833
	TTTTCATCACTGGAACCTATTTCATTAATACTGGAGCCCACTT CATTAGTACTGGAACCTACTTCATTAATATTGCTTGAGCTGGC TTCTTTAAAAACATTTTCTCTAATGTTATTACGGC	834
	TAATGAAGTAGGTTCCA	835
	TGGAACCTACTTCATTA	836
Breast Cancer Leu-1080-Stop TTG to TAG	AAATAGGTTCCAGTGATGAAAACATTCAAGCAGAACTAGGTA GAAACAGAGGGCCAAAATTGAATGCTATGCTTAGATTAGGGG TTTTGCAACCTGAGGTCTATAAACAAAGTCTTCCTGG	837
	CCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCT AATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTA GTTCTGCTTGAATGTTTTCATCACTGGAACCTATTT	838
	GCCAAAATTGAATGCTA	839
	TAGCATTCAATTTTGGC	840
Breast Cancer Leu-1086-Stop TTA to TGA	AAAACATTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAAT TGAATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCT ATAAACAAAGTCTTCCTGGAAGTAATTGTAAGCATCC	841
	GGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCT CAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTG GCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTT	842
	GCTTAGATTAGGGGTTT	843
	AAACCCCTAATCTAAGC	844
Breast Cancer Ser-1130-Stop TCA to TGA	AGCAAGAATATGAAGAAGTAGTTCAGACTGTTAATACAGATTT CTCTCCATATCTGATTTCAGATAACTTAGAACAGCCTATGGGA AGTAGTCATGCATCTCAGGTTTGTTCTGAGACACC	845
	GGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCCATA GGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCT GTATTAACAGTCTGAACTACTTCTTCATATTCTTGCT	846
	TCTGATTTCAGATAACT	847
	AGTTATCTGAAATCAGA	848

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Lys-1183-Arg AAA to AGA	CTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTT TAGCAAAAGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTA GCCCTTTCACCCATACACATTTGGCTCAGGGTTACCG	849
	CGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGG ACTCCTGCTAAGCTCTCCTTTCTGGACGCTTTTGCTAAAAACA GCAGAACTTTCCTTAATGTCATTTTCAGCAAAACTAG	850
	CGTCCAGAAAGGAGAGC	851
	GCTCTCCTTTCTGGACG	852
Breast Cancer Gln-1200-Stop CAG to TAG	AGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTT CACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGG	853
	CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGG GCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCT	854
	ATTTGGCTCAGGGTTAC	855
	GTAACCCTGAGCCAAAT	856
Breast Cancer Arg-1203-Stop CGA to TGA	AAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACA CATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAATTAGA GTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGC	857
	GCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAA TTTCTTGGCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATG GGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTT	858
	AGGGTTACCGAAGAGGG	859
	CCCTCTTCGGTAACCCT	860
Breast Cancer Glu-1214-Stop GAG to TAG	ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAA GAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATGA AGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAAG	861
	CTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCAT CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGT	862
	CCTCAGAAGAGAACTTA	863
	TAAGTTCTCTTCTGAGG	864
Breast Cancer Glu-1219-Asp GAG to GAC	TCAGGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAG AAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCC AACACTTGTTATTTGGTAAAGTAAACAATATACCTTCT	865

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAG CAGGGAAGCTCTTCATC**C**TCACTAGATAAGTTCTCTTCTGAG GACTCTAATTTCTTGGCCCCTCTTCGGTAACCCTGA	866
	TCTAGTGA**G**GATGAAGA	867
	TCTTCATC**C**TCACTAGA	868
Breast Cancer Glu-1221-Stop GAA to TAA	GGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGA GAACTTATCTAGTGAGGAT**G**AAGAGCTTCCCTGCTTCCAACA CTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	869
	ACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTG GAAGCAGGGAAGCTCTT**C**ATCCTCACTAGATAAGTTCTCTTC TGAGGACTCTAATTTCTTGGCCCCTCTTCGGTAACC	870
	GTGAGGAT**G**AAGAGCTT	871
	AAGCTCTT**C**ATCCTCAC	872
Breast Cancer Glu-1250-Stop GAG to TAG	TTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTACTAGGC ATAGCACCGTTGCTACC**G**AGTGTCTGTCTAAGAACACAGAGG AGAATTTATTATCATTGAAGAATAGCTTAAATGACT	873
	AGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTG TTCTTAGACAGACACT**C**GGTAGCAACGGTGCTATGCCTAGTA GACTGAGAAGGTATATTGTTTACTTTACCAAATAA	874
	TTGCTACC**G**AGTGTCTG	875
	CAGACACT**C**GGTAGCAA	876
Breast Cancer Ser-1262-Stop TCA to TAA	CTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACA CAGAGGAGAATTTATTAT**C**ATTGAAGAATAGCTTAAATGACTG CAGTAACCAGGTAATATTGGCAAAGGCATCTCAGGA	877
	TCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCAT TTAAGCTATTCTTCAAT**G**ATAATAAATTCTCCTCTGTGTTCTTA GACAGACACTCGGTAGCAACGGTGCTATGCCTAG	878
	TTTATTAT**C**ATTGAAGA	879
	TCTTCAAT**G**ATAATAAA	880
Breast Cancer Gln-1281-Stop CAG to TAG	TTATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAGGTAA TATTGGCAAAGGCATCT**C**AGGAACATCACCTTAGTGAGGAAA CAAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGCA	881
	TGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTTCCTC ACTAAGGTGATGTTCCT**G**AGATGCCTTTGCCAATATTACCTG GTTACTGCAGTCATTTAAGCTATTCTTCAATGATAA	882

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCATCT**C**AGGAACAT	883
	ATGTTCCT**G**AGATGCCT	884
Breast Cancer Gln-1313-Stop CAG to TAG	GCTAGCTTGTTTTCTTCACAGTGCAGTGAATTGGAAGACTTG ACTGCAAATACAAACACC**C**AGGATCCTTTCTTGATTGGTTCTT CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAG	885
	CTCCCTGGCTTTCAGACTGATGCCTCATTTGTTTGGAAGAAC CAATCAAGAAAGGATCCT**G**GGTGTTTGTATTTGCAGTCAAGT CTTCCAATTCACTGCACTGTGAAGAAAACAAGCTAGC	886
	CAAACACC**C**AGGATCCT	887
	AGGATCCT**G**GGTGTTTG	888
Breast Cancer Ile-1318-Val ATT to GTT	TCACAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC ACCCAGGATCCTTTCTTG**A**TTGGTTCTTCCAAACAAATGAGG CATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACA	889
	TGTCACTCAGACCAACTCCCTGGCTTTCAGACTGATGCCTCA TTTGTTTGGAAGAACCAA**T**CAAGAAAGGATCCTGGGTGTTTG TATTTGCAGTCAAGTCTTCCAATTCACTGCACTGTGA	890
	CTTTCTTG**A**TTGGTTCT	891
	AGAACCAA**T**CAAGAAAG	892
Breast Cancer Gln-1323-Stop CAA to TAA	TTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCTTTC TTGATTGGTTCTTCCAAA**C**AAATGAGGCATCAGTCTGAAAGC CAGGGAGTTGGTCTGAGTGACAAGGAATTGGTTTCAG	893
	CTGAAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTT CAGACTGATGCCTCATTT**G**TTTGGAAGAACCAATCAAGAAAG GATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAA	894
	CTTCCAAA**C**AAATGAGG	895
	CCTCATTT**G**TTTGGAAG	896
Breast Cancer Arg-1347-Gly AGA to GGA	CAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATT GGTTTCAGATGATGAAGAA**A**GAGGAACGGGCTTGGAAGAAA ATAATCAAGAAGAGCAAAGCATGGATTCAAACTTAGGTA	897
	TACCTAAGTTTGAATCCATGCTTTGCTCTTCTTGATTATTTTCT TCCAAGCCCGTTCCTC**T**TTCTTCATCATCTGAAACCAATTCCT TGTCACTCAGACCAACTCCCTGGCTTTCAGACTG	898
	ATGAAGAA**A**GAGGAACG	899
	CGTTCCTC**T**TTCTTCAT	900

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Gln-1395-Stop CAG to TAG	GAAACAAGCGTCTCTGAAGACTGCTCAGGGCTATCCTCTCAG AGTGACATTTTAACCACTCAGGTAAAAAGCGTGTGTGTGTGT GCACATGCGTGTGTGTGGTGTCCTTTGCATTCAGTAG	901
	CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACA CACACACGCTTTTTACCTGAGTGGTTAAAATGTCACTCTGAG AGGATAGCCCTGAGCAGTCTTCAGAGACGCTTGTTTC	902
	TAACCACTCAGGTAAAA	903
	TTTTACCTGAGTGGTTA	904
Breast Cancer Gln-1408-Stop CAG to TAG	TGGTGCCATTTATCGTTTTTGAAGCAGAGGGATACCATGCAA CATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAA GCTGTGTTAGAACAGCATGGGAGCCAGCCTTCTAACA	905
	TGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTA GTTCAGCCATTTCCTGCTGGAGCTTTATCAGGTTATGTTGCAT GGTATCCCTCTGCTTCAAAAACGATAAATGGCACCA	906
	TAAAGCTCCAGCAGGAA	907
	TTCCTGCTGGAGCTTTA	908
Breast Cancer Arg-1443-Gly CGA to GGA Arg-1443-Stop CGA to TGA	AGCCAGCCTTCTAACAGCTACCCTTCCATCATAAGTGACTCT TCTGCCCTTGAGGACCTGCGAAATCCAGAACAAAGCACATCA GAAAAAGGTGTGTATTGTTGGCCAAACACTGATATCT	909
	AGATATCAGTGTTTGGCCAACAATACACACCTTTTTCTGATGT GCTTTGTTCTGGATTTCGCAGGTCCTCAAGGGCAGAAGAGTC ACTTATGATGGAAGGGTAGCTGTTAGAAGGCTGGCT	910
	AGGACCTGCGAAATCCA	911
	TGGATTTCGCAGGTCCT	912
Breast Cancer Ser-1512-Ile AGT to ATT	CAGAATAGAAACTACCCATCTCAAGAGGAGCTCATTAAGGTT GTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	913
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCTGTTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	914
	AGGAGCAACAGCTGGAA	915
	TTCCAGCTGTTGCTCCT	916
Breast Cancer Gln-1538-Stop CAG to TAG	ATCTTTCTAGGTCATCCCCTTCTAAATGCCCATCATTAGATGA TAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAG AAACTACCCATCTCAAGAGGAGCTCATTAAGGTTGT	917

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCT GAAGACTCCCAGAGCAA**C**TGTGCATGTACCACCTATCATCTA ATGATGGGCATTTAGAAGGGGATGACCTAGAAAGAT	918
	CATGCACA**G**TTGCTCTG	919
	CAGAGCAA**C**TGTGCATG	920
Breast Cancer Glu-1541-Stop GAG to TAG	CAGAATAGAAACTACCCATCTCAAGAGGAGCTCATTAAGGTT GTTGATGTGGAGGAGCAA**C**AGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC	921
	GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCT**G**TTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG	922
	AGGAGCAA**C**AGCTGGAA	923
	TTCCAGCT**G**TTGCTCCT	924
Breast Cancer Thr-1561-Ile ACC to ATC	AACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTG GAGGAGCAACAGCTGGAA**G**AGTCTGGGCCACACGATTTGAC GGAAACATCTTACTTGCCAAGGCAAGATCTAGGTAATA	925
	TATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAA ATCGTGTGGCCCAGACT**C**TTCCAGCTGTTGCTCCTCCACATC AACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTT	926
	AGCTGGAA**G**AGTCTGGG	927
	CCCAGACT**C**TTCCAGCT	928
Breast Cancer Tyr-1563-Stop TAC to TAG	TTTGTAATTCAACATTCATCGTTGTGTAAATTAAACTTCTCCCA TTCCTTTCAGAGGGAA**C**CCCTTACCTGGAATCTGGAATCAGC CTCTTCTCTGATGACCCTGAATCTGATCCTTCTGA	929
	TCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATT CCAGATTCCAGGTAAGGG**G**TTCCCTCTGAAAGGAATGGGAG AAGTTTAATTTACACAACGATGAATGTTGAATTACAAA	930
	AGAGGGAA**C**CCCTTACC	931
	GGTAAGGG**G**TTCCCTCT	932
Breast Cancer Leu-1564-Pro CTG to CCG	CAACATTCATCGTTGTGTAAATTAAACTTCTCCCATTCCTTTC AGAGGGAACCCCTTACC**T**GGAATCTGGAATCAGCCTCTTCTC TGATGACCCTGAATCTGATCCTTCTGAAGACAGAGC	933
	GCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAG AGGCTGATTCCAGATTCC**A**GGTAAGGGGTTCCCTCTGAAAG GAATGGGAGAAGTTTAATTTACACAACGATGAATGTTG	934

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCCTTACCTGGAATCTG	935
	CAGATTCCAGGTAAGGG	936
Breast Cancer Gln-1604-Stop CAA to TAA	GCCCCAGAGTCAGCTCGTGTTGGCAACATACCATCTTCAACC TCTGCATTGAAAGTTCCCCAATTGAAAGTTGCAGAATCTGCC CAGAGTCCAGCTGCTGCTCATACTACTGATACTGCTG	937
	CAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCA GATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAGAGGTT GAAGATGGTATGTTGCCAACACGAGCTGACTCTGGGGC	938
	AAGTTCCCCAATTGAAA	939
	TTTCAATTGGGGAACTT	940
Breast Cancer Lys-1606-Glu AAA to GAA	GAGTCAGCTCGTGTTGGCAACATACCATCTTCAACCTCTGCA TTGAAAGTTCCCCAATTGAAAGTTGCAGAATCTGCCCAGAGT CCAGCTGCTGCTCATACTACTGATACTGCTGGGTATA	941
	TATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCT GGGCAGATTCTGCAACTTTCAATTGGGGAACTTTCAATGCAG AGGTTGAAGATGGTATGTTGCCAACACGAGCTGACTC	942
	CCCAATTGAAAGTTGCA	943
	TGCAACTTTCAATTGGG	944
Breast Cancer Met-1628-Thr ATG to ACG	CAGAATCTGCCCAGAGTCCAGCTGCTGCTCATACTACTGATA CTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAG AAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACAA	945
	TTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCC TGCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGT AGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTG	946
	TAATGCAATGGAAGAAA	947
	TTTCTTCCATTGCATTA	948
Breast Cancer Met-1628-Val ATG to GTG	GCAGAATCTGCCCAGAGTCCAGCTGCTGCTCATACTACTGAT ACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGA GAAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACA	949
	TGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCT GCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGTA GTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGC	950
	ATAATGCAATGGAAGAA	951

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCTTCCA**T**TGCATTAT	952
Breast Cancer Pro-1637-Leu CCA to CTA	CTCATACTACTGATACTGCTGGGTATAATGCAATGGAAGAAA GTGTGAGCAGGGAGAAGC**C**AGAATTGACAGCTTCAACAGAA AGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCT	953
	AGGCCAGACACCACCATGGACATTCTTTTGTTGACCCTTTCT GTTGAAGCTGTCAATTCT**G**GCTTCTCCCTGCTCACACTTTCTT CCATTGCATTATACCCAGCAGTATCAGTAGTATGAG	954
	GGAGAAGC**C**AGAATTGA	955
	TCAATTCT**G**GCTTCTCC	956
Breast Cancer Met-1652-Ile ATG to ATA	GAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAAAGGG TCAACAAAAGAATGTCCAT**G**GTGGTGTCTGGCCTGACCCCAG AAGAATTTGTGAGTGTATCCATATGTATCTCCCTAATG	957
	CATTAGGGAGATACATATGGATACACTCACAAATTCTTCTGG GGTCAGGCCAGACACCAC**C**ATGGACATTCTTTTGTTGACCCT TTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTC	958
	ATGTCCAT**G**GTGGTGTC	959
	GACACCAC**C**ATGGACAT	960
Breast Cancer Glu-1694-Stop GAG to TAG	CACTTCCTGATTTTGTTTTCAACTTCTAATCCTTTGAGTGTTTT TCATTCTGCAGATGCT**G**AGTTTGTGTGTGAACGGACACTGAA ATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG	961
	CTACCCATTTTCCTCCCGCAATTCCTAGAAAATATTTCAGTGT CCGTTCACACACAAACT**C**AGCATCTGCAGAATGAAAAACACT CAAAGGATTAGAAGTTGAAAACAAAATCAGGAAGTG	962
	CAGATGCT**G**AGTTTGTG	963
	CACAAACT**C**AGCATCTG	964
Breast Cancer Gly-1706-Glu GGA to GAA	GTGTTTTTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGA CACTGAAATATTTTCTAG**G**AATTGCGGGAGGAAAATGGGTAG TTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT	965
	AGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACCC ATTTTCCTCCCGCAATT**C**CTAGAAAATATTTCAGTGTCCGTTC ACACACAAACTCAGCATCTGCAGAATGAAAAACAC	966
	TTTTCTAG**G**AATTGCGG	967
	CCGCAATT**C**CTAGAAAA	968

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Ala-1708-Glu GCG to GAG	TTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAATTG**C**GGGAGGAAAATGGGTAGTTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCTCCTCCC	969
	GGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACCCATTTTCCTCCC**G**CAATTCCTAGAAAATATTTCAGTGTCCGTTCACACACAAACTCAGCATCTGCAGAATGAA	970
	AGGAATTG**C**GGGAGGAA	971
	TTCCTCCC**G**CAATTCCT	972
Breast Cancer Val-1713-Ala GTA to GCA	CTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGG**T**AGTTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCTCCTCCCTTTAACACCTCAGAA	973
	TTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACT**A**CCCATTTTCCTCCCGCAATTCCTAGAAAATATTTCAGTGTCCGTTCACACACAAACTCAG	974
	AAAATGGG**T**AGTTAGCT	975
	AGCTAACT**A**CCCATTTT	976
Breast Cancer Trp-1718-Stop TGG to TAG	AACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAGTTAGCTATTTCT**G**TAAGTATAATACTATTTCTCCCCTCCTCCCTTTAACACCTCAGAATTGCATTTTTACACC	977
	GGTGTAAAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATACTTA**C**AGAAATAGCTAACTACCCATTTTCCTCCCGCAATTCCTAGAAAATATTTCAGTGTCCGTT	978
	CTATTTCT**G**TAAGTATA	979
	TATACTTA**C**AGAAATAG	980
Breast Cancer Glu-1725-Stop GAA to TAA	TTCTGCTGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGGTGACCCAGTCTATTAAA**G**AAAGAAAAATGCTGAATGAGGTAAGTACTTGATGTTACAAACTAACCAGAGATATTCATT	981
	AATGAATATCTCTGGTTAGTTTGTAACATCAAGTACTTACCTCATTCAGCATTTTTCTTT**C**TTTAATAGACTGGGTCACCCCTAAAGAGATCATAGAAAAGACAGGTTACATACAGCAGAA	982
	CTATTAAA**G**AAAGAAAA	983
	TTTTCTTT**C**TTTAATAG	984
Breast Cancer Lys-1727-Stop AAA to TAA	TGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGGTGACCCAGTCTATTAAAGAAAGA**A**AAATGCTGAATGAGGTAAGTACTTGATGTTACAAACTAACCAGAGATATTCATTCAGTCA	985

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGACTGAATGAATATCTCTGGTTAGTTTGTAACATCAAGTACT TACCTCATTCAGCATTTT**T**TCTTTCTTTAATAGACTGGGTCACC CCTAAAGAGATCATAGAAAAGACAGGTTACATACA	986
	AAGAAAGA**A**AAATGCTG	987
	CAGCATTTT**T**TCTTTCTT	988
Breast Cancer Pro-1749-Arg CCA to CGA	TCTTTCAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATG GAAGAAACCACCAAGGTC**C**AAAGCGAGCAAGAGAATCCCAG GACAGAAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAA	989
	TTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGG GATTCTCTTGCTCGCTTT**G**GACCTTGGTGGTTTCTTCCATTGA CCACATCTCCTCTGACTTCAAAATCATGCTGAAAGA	990
	CCAAGGTC**C**AAAGCGAG	991
	CTCGCTTT**G**GACCTTGG	992
Breast Cancer Arg-1751-Stop CGA to TGA	CAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAAGA AACCACCAAGGTCCAAAG**C**GAGCAAGAGAATCCCAGGACAG AAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAAATCTC	993
	GAGATTTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGT CCTGGGATTCTCTTGCTC**G**CTTTGGACCTTGGTGGTTTCTTC CATTGACCACATCTCCTCTGACTTCAAAATCATGCTG	994
	GTCCAAAG**C**GAGCAAGA	995
	TCTTGCTC**G**CTTTGGAC	996
Breast Cancer Gln-1756-Stop CAG to TAG	GTCAGAGGAGATGTGGTCAATGGAAGAAACCACCAAGGTCC AAAGCGAGCAAGAGAATCC**C**AGGACAGAAAGGTAAAGCTCC CTCCCTCAAGTTGACAAAAATCTCACCCCACCACTCTGT	997
	ACAGAGTGGTGGGGTGAGATTTTTGTCAACTTGAGGGAGGG AGCTTTACCTTTCTGTCCT**G**GGATTCTCTTGCTCGCTTTGGA CCTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGAC	998
	GAGAATCC**C**AGGACAGA	999
	TCTGTCCT**G**GGATTCTC	1000
Breast Cancer Met-1775-Arg ATG to AGG	CTCTCTTCTTCCAGATCTTCAGGGGGCTAGAAATCTGTTGCT ATGGGCCCTTCACCAACA**T**GCCCACAGGTAAGAGCCTGGGA GAACCCCAGAGTTCCAGCACCAGCCTTTGTCTTACATA	1001
	TATGTAAGACAAAGGCTGGTGCTGGAACTCTGGGGTTCTCCC AGGCTCTTACCTGTGGGC**A**TGTTGGTGAAGGGCCCATAGCA ACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAG	1002

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACCAACATGCCCACAG	1003
	CTGTGGGCATGTTGGTG	1004
Breast Cancer Trp-1782-Stop TGG to TGA	AGTATGCAGATTACTGCAGTGATTTTACATCTAAATGTCCATT TTAGATCAACTGGAATGGATGGTACAGCTGTGTGGTGCTTCT GTGGTGAAGGAGCTTTCATCATTCACCCTTGGCACA	1005
	TGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGC ACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGA CATTTAGATGTAAAATCACTGCAGTAATCTGCATACT	1006
	CTGGAATGGATGGTACA	1007
	TGTACCATCCATTCCAG	1008
Breast Cancer Gln-1785-His CAG to CAT	ATTACTGCAGTGATTTTACATCTAAATGTCCATTTTAGATCAAC TGGAATGGATGGTACAGCTGTGTGGTGCTTCTGTGGTGAAG GAGCTTTCATCATTCACCCTTGGCACAGTAAGTATT	1009
	AATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCAC CACAGAAGCACCACACAGCTGTACCATCCATTCCAGTTGATC TAAAATGGACATTTAGATGTAAAATCACTGCAGTAAT	1010
	ATGGTACAGCTGTGTGG	1011
	CCACACAGCTGTACCAT	1012
Breast Cancer Glu-1794-Asp GAG to GAT	GTCCATTTTAGATCAACTGGAATGGATGGTACAGCTGTGTGG TGCTTCTGTGGTGAAGGAGCTTTCATCATTCACCCTTGGCAC AGTAAGTATTGGGTGCCCTGTCAGAGAGGGAGGACAC	1013
	GTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCC AAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCACA CAGCTGTACCATCCATTCCAGTTGATCTAAAATGGAC	1014
	GTGAAGGAGCTTTCATC	1015
	GATGAAAGCTCCTTCAC	1016
Breast Cancer Arg-1835-Stop CGA to TGA	CTCTGCTTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGT GAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGT AGCACTCTACCAGTGCCAGGAGCTGGACACCTACCTGA	1017
	TCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACA CTGTCCAACACCCACTCTCGGGTCACCACAGGTGCCTCACA CATCTGCCCAATTGCTGGAGACAGAGAACACAAGCAGAG	1018
	TGGTGACCCGAGAGTGG	1019
	CCACTCTCGGGTCACCA	1020

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast Cancer Trp-1837-Arg TGG to CGG	TTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCA CCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGTAGCACT CTACCAGTGCCAGGAGCTGGACACCTACCTGATACCCC	1021
	GGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGT GCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTGC CTCACACATCTGCCCAATTGCTGGAGACAGAGAACACAA	1022
	CCCGAGAGTGGGTGTTG	1023
	CAACACCCACTCTCGGG	1024
Breast Cancer Trp-1837-Stop TGG to TAG	TGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCAC CTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGTAGCACTC TACCAGTGCCAGGAGCTGGACACCTACCTGATACCCCA	1025
	TGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAG TGCTACACTGTCCAACACCCACTCTCGGGTCACCACAGGTG CCTCACACATCTGCCCAATTGCTGGAGACAGAGAACACA	1026
	CCGAGAGTGGGTGTTGG	1027
	CCAACACCCACTCTCGG	1028

Table 15

BRCA2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer PHE32LEU TTT to CTT	GTTAAAACTAAGGTGGGATTTTTTTTTTAAATAGATTTAGGAC CAATAAGTCTTAATTGGTTTGAAGAACTTTCTTCAGAAGCTCC ACCCTATAATTCTGAACCTGCAGAAGAATCTGAAC	1029
	GTTCAGATTCTTCTGCAGGTTCAGAATTATAGGGTGGAGCTT CTGAAGAAAGTTCTTCAAACCAATTAAGACTTATTGGTCCTAA ATCTATTTAAAAAAAAAATCCCACCTTAGTTTTAAC	1030
	TTAATTGGTTTGAAGAA	1031
	TTCTTCAAACCAATTAA	1032
Breast cancer TYR42CYS TAT to TGT	TAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTC TTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATC TGAACATAAAAACAACAATTACGAACCAAACCTATT	1033

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATAGGTTTGGTTCGTAATTGTTGTTTTTATGTTCAGATTCTTC TGCAGGTTCAGAATTA**T**AGGGTGGAGCTTCTGAAGAAAGTTC TTCAAACCAATTAAGACTTATTGGTCCTAAATCTA	1034
	TCCACCCT**A**TAATTCTG	1035
	CAGAATTA**T**AGGGTGGA	1036
Breast cancer LYS53ARG AAA to AGA	AAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC AGAAGAATCTGAACATA**A**AAACAACAATTACGAACCAAACCTA TTTAAAACTCCACAAAGGAAACCATCTTATAATCA	1037
	TGATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAGGTTTG GTTCGTAATTGTTGTTT**T**TATGTTCAGATTCTTCTGCAGGTTC AGAATTATAGGGTGGAGCTTCTGAAGAAAGTTCTT	1038
	TGAACATA**A**AAACAACA	1039
	TGTTGTTT**T**TATGTTCA	1040
Breast cancer Phe81Leu TTC to CTC	CTATTTAAAACTCCACAAAGGAAACCATCTTATAATCAGCTGG CTTCAACTCCAATAATA**T**TCAAAGAGCAAGGGCTGACTCTGC CGCTGTACCAATCTCCTGTAAAAGAATTAGATAAAT	1041
	ATTTATCTAATTCTTTTACAGGAGATTGGTACAGCGGCAGAGT CAGCCCTTGCTCTTTGA**A**TATTATTGGAGTTGAAGCCAGCTG ATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAG	1042
	CAATAATA**T**TCAAAGAG	1043
	CTCTTTGA**A**TATTATTG	1044
Breast cancer TRP194TERM TGG to TAG	GTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGAGG TGGATCCTGATATGTCTT**G**GTCAAGTTCTTTAGCTACACCACC CACCCTTAGTTCTACTGTGCTCATAGGTAATAATAG	1045
	CTATTATTACCTATGAGCACAGTAGAACTAAGGGTGGGTGGT GTAGCTAAAGAACTTGAC**C**AAGACATATCAGGATCCACCTCA GCTCCTAGACTTTCAGAAATATGTTTTGGTGTCTGAC	1046
	TATGTCTT**G**GTCAAGTT	1047
	AACTTGAC**C**AAGACATA	1048
Breast cancer PRO201ARG CCA to CGA	CTGAAAGTCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGT CAAGTTCTTTAGCTACAC**C**ACCCACCCTTAGTTCTACTGTGCT CATAGGTAATAATAGCAAATGTGTATTTACAAGAAA	1049
	TTTCTTGTAAATACACATTTGCTATTATTACCTATGAGCACAGT AGAACTAAGGGTGGGT**G**GTGTAGCTAAAGAACTTGACCAAGA CATATCAGGATCCACCTCAGCTCCTAGACTTTCAG	1050

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGCTACAC**C**ACCCACCC	1051
	GGGTGGGT**G**GTGTAGCT	1052
Breast cancer Pro222Ser CCT to TCT	ACAATACACATAAATTTTTATCTTACAGTCAGAAATGAAGAG CATCTGAAACTGTATTT**C**CTCATGATACTACTGCTGTAAGTAA ATATGACATTGATTAGACTGTTGAAATTGCTAACA	1053
	TGTTAGCAATTTCAACAGTCTAATCAATGTCATATTTACTTACA GCAGTAGTATCATGAG**G**AAATACAGTTTCAGATGCTTCTTCAT TTCTGACTGTAAGATAAAAATTTATGTGTATTGT	1054
	CTGTATTT**C**CTCATGAT	1055
	ATCATGAG**G**AAATACAG	1056
Breast cancer Leu-414-Term TTG to TAG	AATGGTCTCAACTAACCCTTTCAGGTCTAAATGGAGCCCAGA TGGAGAAAATACCCCTAT**T**GCATATTTCTTCATGTGACCAAAA TATTTCAGAAAAAGACCTATTAGACACAGAGAACAA	1057
	TTGTTCTCTGTGTCTAATAGGTCTTTTTCTGAAATATTTTGGTC ACATGAAGAAATATGC**A**ATAGGGGTATTTTCTCCATCTGGGC TCCATTTAGACCTGAAAGGGTTAGTTGAGACCATT	1058
	ACCCCTAT**T**GCATATTT	1059
	AAATATGC**A**ATAGGGGT	1060
Breast cancer, male Cys554Trp TGT to TGG	AGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACA GAAGGAGGACTCCTTATG**T**CCAAATTTAATTGATAATGGAAG CTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTG	1061
	CAAAGCTACAGAATTCTGTGTGGTGGTGGCTGGCCAGCTTC CATTATCAATTAAATTTGG**A**CATAAGGAGTCCTCCTTCTGTGA GCAAACAGTATGTATTTCCAGTCCACTTTCAGAGGCT	1062
	TCCTTATG**T**CCAAATTT	1063
	AAATTTGG**A**CATAAGGA	1064
Breast cancer Lys944Term AAA to TAA	AACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAA GCAACCCAAGTGTCAATT**A**AAAAAGATTTGGTTTATGTTCTTG CAGAGGAGAACAAAAATAGTGTAAAGCAGCATATAA	1065
	TTATATGCTGCTTTACACTATTTTTGTTCTCCTCTGCAAGAAC ATAAACCAAATCTTTTT**T**AATTGACACTTGGGTTGCTTGTTTAT CACCTGTGTCTCCATATAAAACCATGGTAGAGTT	1066
	TGTCAATT**A**AAAAAGAT	1067
	ATCTTTTT**T**AATTGACA	1068

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer, male Glu1320Term GAA to TAA	ATGACTACTGGCACTTTTGTTGAAGAAATTACTGAAAATTACAAGAGAAATACTGAAAAT**G**AAGATAACAAATATACTGCTGCCAGTAGAAATTCTCATAACTTAGAATTTGATGGCAGTG	1069
	CACTGCCATCAAATTCTAAGTTATGAGAATTTCTACTGGCAGCAGTATATTTGTTATCTT**C**ATTTTCAGTATTTCTCTTGTAATTTTCAGTAATTTCTTCAACAAAAGTGCCAGTAGTCAT	1070
	CTGAAAAT**G**AAGATAAC	1071
	GTTATCTT**C**ATTTTCAG	1072
Breast cancer Glu1876Term GAA to TAA	CATGAAACAATTAAAAAAGTGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAG**G**AAAACAACGAGAATAAATCAAAAATTTGCCAAACGAAAATTATGGCAGGTTGTTACGAGG	1073
	CCTCGTAACAACCTGCCATAATTTTCGTTTGGCAAATTTTTGATTTATTCTCGTTGTTTT**C**CTTAATTACTTTACTGAAACTGTCTGTAAATATGTCTTTCACTTTTTTAATTGTTTCATG	1074
	TAATTAAG**G**AAAACAAC	1075
	GTTGTTTT**C**CTTAATTA	1076
Breast cancer Ser1882Term TCA to TAA	TGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGAAAACAACGAGAATAAAT**C**AAAAATTTGCCAAACGAAAATTATGGCAGGTTGTTACGAGGCATTGGATGATTCAGAGGA	1077
	TCCTCTGAATCATCCAATGCCTCGTAACAACCTGCCATAATTTTCGTTTGGCAAATTTTT**G**ATTTATTCTCGTTGTTTTCCTTAATTACTTTACTGAAACTGTCTGTAAATATGTCTTTCA	1078
	GAATAAAT**C**AAAAATTT	1079
	AAATTTTT**G**ATTTATTC	1080
Breast cancer Glu1953Term GAA to TAA	AACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAAATATCACCTTGTGATGTTAGTTTG**G**AAACTTCAGATATATGTAAATGTAGTATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAA	1081
	TTGCAGATGAGACTGACTTATGAAGCTTCCCTATACTACATTTACATATATCTGAAGTTT**C**CAAACTAACATCACAAGGTGATATTTTAGAAACTTTCTCCAATCCAGACATATTTTGGTT	1082
	TTAGTTTG**G**AAACTTCA	1083
	TGAAGTTT**C**CAAACTAA	1084
Breast cancer Ser1970Term TCA to TAA	TTAGTTTGGAAACTTCAGATATATGTAAATGTAGTATAGGGAAGCTTCATAAGTCAGTCT**C**ATCTGCAAATACTTGTGGGATTTTTAGCACAGCAAGTGGAAAATCTGTCCAGGTATCAGA	1085

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGATACCTGGACAGATTTTCCACTTGCTGTGCTAAAAATCC CACAAGTATTTGCAGAT**G**AGACTGACTTATGAAGCTTCCCTAT ACTACATTTACATATATCTGAAGTTTCCAAACTAA	1086
	GTCAGTCT**C**ATCTGCAA	1087
	TTGCAGAT**G**AGACTGAC	1088
Breast cancer Gln1987Term CAG to TAG	AAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAG CAAGTGGAAAATCTGTC**C**AGGTATCAGATGCTTCATTACAAAA CGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTA	1089
	TACTATCTTCTATTTCAGAAAACACTTGTCTTGCGTTTTGTAAT GAAGCATCTGATACCT**G**GACAGATTTTCCACTTGCTGTGCTA AAAATCCCACAAGTATTTGCAGATGAGACTGACTT	1090
	AATCTGTC**C**AGGTATCA	1091
	TGATACCT**G**GACAGATT	1092
Breast cancer Ala2466Val GCA to GTA	AAAATAAGATTAATGACAATGAGATTCATCAGTTTAACAAAAA CAACTCCAATCAAGCAG**C**AGCTGTAACTTTCACAAAGTGTGA AGAAGAACCTTTAGGTATTGTATGACAATTTGTGTG	1093
	CACACAAATTGTCATACAATACCTAAAGGTTCTTCTTCACACT TTGTGAAAGTTACAGCT**G**CTGCTTGATTGGAGTTGTTTTTGTT AAACTGATGAATCTCATTGTCATTAATCTTATTTT	1094
	TCAAGCAG**C**AGCTGTAA	1095
	TTACAGCT**G**CTGCTTGA	1096
Breast cancer Arg2520Term CGA to TGA	AGGCAACGCGTCTTTCCACAGCCAGGCAGTCTGTATCTTGCA AAAACATCCACTCTGCCT**C**GAATCTCTCTGAAAGCAGCAGTA GGAGGCCAAGTCCCCTCTGCGTGTCCTCATAAACAGG	1097
	CCTGTTTATGAGGACACGCAGAGGGGACTTGGCCTCCTACT GCTGCTTTCAGAGAGATTC**G**AGGCAGAGTGGATGTTTTTGCA AGATACAGACTGCCTGGCTGTGGAAAGACGCGTTGCCT	1098
	CTCTGCCT**C**GAATCTCT	1099
	AGAGATTC**G**AGGCAGAG	1100
Breast cancer Gln2714Term CAA to TAA	ATTTCATTGAGCGCAAATATATCTGAAACTTCTAGCAATAAAA CTAGTAGTGCAGATACC**C**AAAAAGTGGCCATTATTGAACTTA CAGATGGGTGGTATGCTGTTAAGGCCCAGTTAGATC	1101
	GATCTAACTGGGCCTTAACAGCATACCACCCATCTGTAAGTT CAATAATGGCCACTTTTT**G**GGTATCTGCACTACTAGTTTTATT GCTAGAAGTTTCAGATATATTTGCGCTCAATGAAAT	1102

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGATACCCAAAAAGTG	1103
	CACTTTTTGGGTATCTG	1104
Breast cancer Leu2776Term TTA to TGA	CAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAG CCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTT GGTAAAAATCAGTCATTGATTCAGTTAAATTCTAGA	1105
	TCTAGAATTTAACTGAATCAATGACTGATTTTTACCAAGAGTG CAAATTAATTTACCTTTAACATAAGAGATTCTGGGGCTTCAAG AGGTGTACAGGCATCAGGAGAGCCCACCAGTTCTG	1106
	TCTTATGTTAAAGATTT	1107
	AAATCTTTAACATAAGA	1108
Breast cancer Gln2893Term CAG to TAG	CCTTTTGTTTTCTTAGAAAACACAACAAAACCATATTTACCATC ACGTGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGG TGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAG	1109
	CTGCTGCATTCTTCACTGCTTCATAAAGCTCTGCACCATCTTG CAAAGCACGAACTTGCTGTCTTGTTAGTGCACGTGATGGTAA ATATGGTTTTGTTGTGTTTTCTAAGAAAACAAAAGG	1110
	TAACAAGACAGCAAGTT	1111
	AACTTGCTGTCTTGTTA	1112
Breast cancer Ala2951Thr GCC to ACC	AATCACAGGCAAATGTTGAATGATAAGAAACAAGCTCAGATC CAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAG GAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGA	1113
	TCCACACGGTTGTGACATCCCTTGATAAACCTTGTTCCTTTTG TTCAGCAGATTCCATGGCCTTCCTAATTTCCAACTGGATCTGA GCTTGTTTCTTATCATTCAACATTTGCCTGTGATT	1114
	TTAGGAAGGCCATGGAA	1115
	TTCCATGGCCTTCCTAA	1116
Breast cancer Met3118Thr ATG to ACG	ACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGA CATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAG TGGCGACCAGAATCCAAATCAGGCCTTCTTACTTT	1117
	AAAGTAAGAAGGCCTGATTTGGATTCTGGTCGCCACTGGAG GTTGCTTGCAGCAATTAACATATGAGGCTTAATAATGTCCTCA TTAAGGTCTATCCAAAACTTTATTGCCAGTAAATTGT	1118
	GCCTCATATGTTAATTG	1119
	CAATTAACATATGAGGC	1120

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Breast cancer Thr3401Met ACG to ATG	GACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATT	1121
	AATGCTTAGATATATTTTTTAGTTGTAATTGTGTCCTGCTTATTTTTCTCACATTCTTCCGTACTGGCCTGGGAACTCTCCTGTTCTTTGATCAGAGATGTAGTACAACGTCGTTTCAGTC	1122
	GGCCAGTACGGAAGAAT	1123
	ATTCTTCCGTACTGGCC	1124
Breast cancer Ile3412Val ATT to GTT	AAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAGCAGGACACAATTACAACTAAAAAATATATCTAAGCATTTGCAAAGGCGACAATAAATTATTGACGCTTAA	1125
	TTAAGCGTCAATAATTTATTGTCGCCTTTGCAAATGCTTAGATATATTTTTTAGTTGTAATTGTGTCCTGCTTATTTTTCTCACATTCTTCCGTACTGGCCTGGGAACTCTCCTGTTCTTT	1126
	AGGACACAATTACAACT	1127
	AGTTGTAATTGTGTCCT	1128

EXAMPLE 9
Cystic Fibrosis - CFTR

Cystic fibrosis is a lethal disease affecting approximately one in 2,500 live Caucasian births and is the most common autosomal recessive disease in Caucasians. Patients with this disease have reduced chloride ion permeability in the secretory and absorptive cells of organs with epithelial cell linings, including the airways, pancreas, intestine, sweat glands and male genital tract. This, in turn, reduces the transport of water across the epithelia. The lungs and the GI tract are the predominant organ systems affected in this disease and the pathology is characterized by blocking of the respiratory and GI tracts with viscous mucus. The chloride impermeability in affected tissues is due to mutations in a specific chloride channel, the cystic fibrosis transmembrane conductance regulator protein (CFTR), which prevents normal passage of chloride ions through the cell membrane (Welsh et al., Neuron, 8:821-829 (1992)). Damage to the lungs due to mucus blockage, frequent bacterial infections and inflammation is the primary cause of morbidity and mortality in CF patients and, although maintenance therapy has improved the quality of patients' lives, the median age at death is still only around 30 years. There is no effective treatment for the disease, and therapeutic research is focused on gene therapy using

exogenous transgenes in viral vectors and/or activating the defective or other chloride channels in the cell membrane to normalize chloride permeability (Tizzano et al., J. Pediat., 120:337-349 (1992)). However, the death of a teenage patient treated with an adenovirus vector carrying an exogenous CFTR gene in clinical trials in the late 1990's has impacted this area of research.

The oligonucleotides of the invention for correction of the CFTR gene are attached as a table.

Table 16
CFTR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Ala46Asp GCT to GAT	AAGGATACAGACAGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTGATTCTG**C**TGACAATCTATCTGAAAAATTGGAAAGGTATGTTCATGTACATTGTTTAGTTGAAGAGAG	1129
	CTCTCTTCAACTAAACAATGTACATGAACATACCTTTCCAATTTTTCAGATAGATTGTCA**G**CAGAATCAACAGAAGGGATTTGGTATATGTCTGACAATTCCAGGCGCTGTCTGTATCCTT	1130
	TGATTCTG**C**TGACAATC	1131
	GATTGTCA**G**CAGAATCA	1132
Cystic fibrosis Ser50Tyr TCT to TAT	AGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTGATTCTGCTGACAATCTAT**C**TGAAAAATTGGAAAGGTATGTTCATGTACATTGTTTAGTTGAAGAGAGAAATTCATATTA	1133
	TAATATGAATTTCTCTCTTCAACTAAACAATGTACATGAACATACCTTTCCAATTTTTCA**G**ATAGATTGTCAGCAGAATCAACAGAAGGGATTTGGTATATGTCTGACAATTCCAGGCGCT	1134
	CAATCTAT**C**TGAAAAAT	1135
	ATTTTTCA**G**ATAGATTG	1136
Congenital absence of vas deferens Glu56Lys GAA-AAA	AGGACAACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTGCAGA**G**AATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGAT	1137
	ATCGCCGAAGGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTCTATCCCATT**C**TCTGCAAAAGAATAAAAAGTGGGACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT	1138
	TTTGCAGA**G**AATGGGAT	1139
	ATCCCATT**C**TCTGCAAA	1140

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Trp57Gly TGG to GGG	AGGACAACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTGCAGA**G**AATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGAT	1141
	ATCGCCGAAGGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTCTATCCCATT**C**TCTGCAAAAGAATAAAAAGTGGGACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT	1142
	TTTGCAGA**G**AATGGGAT	1143
	ATCCCATT**C**TCTGCAAA	1144
Cystic fibrosis Trp57Term TGG to TGA	AACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTGCAGAGAATG**G**GATAGAGAGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTT	1145
	AAAACATCGCCGAAGGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTCTATC**C**CATTCTCTGCAAAAGAATAAAAAGTGGGACCAATAAGTTGCATGTGCAAATATTTTAGTT	1146
	AGAGAATG**G**GATAGAGA	1147
	TCTCTATC**C**CATTCTCT	1148
Congenital absence of vas deferens Asp58Asn GAT to AAT	ACTAAAATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTGCAGAGAATGG**G**ATAGAGAGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTT	1149
	AAAAACATCGCCGAAGGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTCTAT**C**CCATTCTCTGCAAAAGAATAAAAAGTGGGACCAATAAGTTGCATGTGCAAATATTTTAGT	1150
	GAGAATGG**G**ATAGAGAG	1151
	CTCTCTAT**C**CCATTCTC	1152
Cystic fibrosis Glu60Term GAG to TAG	ATATTTGCACATGCAACTTATTGGTCCCACTTTTTATTCTTTTGCAGAGAATGGGATAGA**G**AGCTGGCTTCAAAGAAAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTTCTGGA	1153
	TCCAGAAAAACATCGCCGAAGGGCATTAATGAGTTTAGGATTTTTCTTTGAAGCCAGCT**C**TCTATCCCATTCTCTGCAAAAGAATAAAAAGTGGGACCAATAAGTTGCATGTGCAAATAT	1154
	GGGATAGA**G**AGCTGGCT	1155
	AGCCAGCT**C**TCTATCCC	1156

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Pro67Leu CCT to CTT	GGTCCCACTTTTTATTCTTTTGCAGAGAATGGGATAGAGAGC TGGCTTCAAAGAAAAATC**C**TAAACTCATTAATGCCCTTCGGC GATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTT	1157
	AAGATTCCATAGAACATAAATCTCCAGAAAAAACATCGCCGAA GGGCATTAATGAGTTTA**G**GATTTTTCTTTGAAGCCAGCTCTCT ATCCCATTCTCTGCAAAAGAATAAAAAGTGGGACC	1158
	GAAAAATC**C**TAAACTCA	1159
	TGAGTTTA**G**GATTTTTC	1160
Cystic fibrosis Arg74Trp CGG to TGG	TGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCT AAACTCATTAATGCCCTT**C**GGCGATGTTTTTTCTGGAGATTTA TGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGA	1161
	TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCC**G**AAGGGCATTAATGAGTTTAGGATT TTTCTTTGAAGCCAGCTCTCTATCCCATTCTCTGCA	1162
	ATGCCCTT**C**GGCGATGT	1163
	ACATCGCC**G**AAGGGCAT	1164
Congenital absence of vas deferens ARG75GLN CGA to CAA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGC**G**ATGTTTTTTCTGGAGATTTATGTT CTATGGAATCTTTTTATATTTAGGGGTAAGGATCTC	1165
	GAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACAT**C**GCCGAAGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC	1166
	CCTTCGGC**G**ATGTTTTT	1167
	AAAAACAT**C**GCCGAAGG	1168
Cystic fibrosis Arg75Leu CGA to CTA	GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGC**G**ATGTTTTTTCTGGAGATTTATGTT CTATGGAATCTTTTTATATTTAGGGGTAAGGATCTC	1169
	GAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACAT**C**GCCGAAGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC	1170
	CCTTCGGC**G**ATGTTTTT	1171
	AAAAACAT**C**GCCGAAGG	1172
Cystic fibrosis Arg75Term CGA to TGA	AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAA CTCATTAATGCCCTTCGG**C**GATGTTTTTTCTGGAGATTTATGT TCTATGGAATCTTTTTATATTTAGGGGTAAGGATCT	1173

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAA TCTCCAGAAAAAACATC**G**CCGAAGGGCATTAATGAGTTTAGG ATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTCT	1174
	CCCTTCGG**C**GATGTTTT	1175
	AAAACATC**G**CCGAAGGG	1176
Cystic fibrosis Gly85Glu GGA to GAA	AAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTTTCTG GAGATTTATGTTCTATG**G**AATCTTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1177
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATT**C**CATAGAACATAAATCTCCAGAAAAA ACATCGCCGAAGGGCATTAATGAGTTTAGGATTTT	1178
	GTTCTATG**G**AATCTTTT	1179
	AAAAGATT**C**CATAGAAC	1180
Cystic fibrosis Gly85Val GGA to GTA	AAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTTTCTG GAGATTTATGTTCTATG**G**AATCTTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT	1181
	AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATT**C**CATAGAACATAAATCTCCAGAAAAA ACATCGCCGAAGGGCATTAATGAGTTTAGGATTTT	1182
	GTTCTATG**G**AATCTTTT	1183
	AAAAGATT**C**CATAGAAC	1184
Cystic fibrosis Leu88Ser TTA to TCA	AACTCATTAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTAT GTTCTATGGAATCTTTT**T**ATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT	1185
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATAT**A**AAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAAGGGCATTAATGAGTT	1186
	AATCTTTT**T**ATATTTAG	1187
	CTAAATAT**A**AAAAGATT	1188
Cystic fibrosis Phe87Leu TTT to CTT	CCTAAACTCATTAATGCCCTTCGGCGATGTTTTTTCTGGAGAT TTATGTTCTATGGAATC**T**TTTTATATTTAGGGGTAAGGATCTC ATTTGTACATTCATTATGTATCACATAACTATATG	1189
	CATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCT TACCCCTAAATATAAAA**A**GATTCCATAGAACATAAATCTCCAG AAAAAACATCGCCGAAGGGCATTAATGAGTTTAGG	1190

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGGAATCTTTTTATAT	1191
	ATATAAAAAGATTCCAT	1192
Cystic fibrosis Leu88Term TTA to TGA	AACTCATTAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGATCTCATTTGTACATTCATTATGTATCACATAACTATATGCATT	1193
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAAAACATCGCCGAAGGGCATTAATGAGTT	1194
	AATCTTTTTATATTTAG	1195
	CTAAATATAAAAAGATT	1196
Cystic fibrosis Leu88Term TTA to TAA	AACTCATTAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGATCTCATTTGTACATTCATTATGTATCACATAACTATATGCATT	1197
	AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAAAACATCGCCGAAGGGCATTAATGAGTT	1198
	AATCTTTTTATATTTAG	1199
	CTAAATATAAAAAGATT	1200
Cystic fibrosis Gly91Arg GGG to AGG	AATGCCCTTCGGCGATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGATCTCATTTGTACATTCATTATGTATCACATAACTATATGCATTTTTGTGAT	1201
	ATCACAAAAATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAAAACATCGCCGAAGGGCATT	1202
	TATATTTAGGGGTAAGG	1203
	CCTTACCCCTAAATATA	1204
Cystic fibrosis Gln98Arg CAG to CGG	AATAAATGAAATTTAATTTCTCTGTTTTTCCCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTC	1205
	GAGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAAATTTCATTTATT	1206
	AGCAGTACAGCCTCTCT	1207
	AGAGAGGCTGTACTGCT	1208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Gln98Term CAG-TAG	AAATAAATGAAATTTAATTTCTCTGTTTTTCCCCTTTTGTAGGAAGTCACCAAAGCAGTA**C**AGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCT	1209
	AGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCT**G**TACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAAATTTCATTTATTT	1210
	AAGCAGTA**C**AGCCTCTC	1211
	GAGAGGCT**G**TACTGCTT	1212
Cystic fibrosis Ser108Phe TCC to TTC	CCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTT**C**CTATGACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATG	1213
	CATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCATAG**G**AAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGG	1214
	CATAGCTT**C**CTATGACC	1215
	GGTCATAG**G**AAGCTATG	1216
Cystic fibrosis Tyr109Cys TAT to TGT	TTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCT**A**TGACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCT	1217
	AGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCA**T**AGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAA	1218
	AGCTTCCT**A**TGACCCGG	1219
	CCGGGTCA**T**AGGAAGCT	1220
Cystic fibrosis Asp110His GAC to CAC	TTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTAT**G**ACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTC	1221
	GAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGT**C**ATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAA	1222
	CTTCCTAT**G**ACCCGGAT	1223
	ATCCGGGT**C**ATAGGAAG	1224

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Congenital absence of vas deferens Pro111Leu CCG to CTG	AGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC**C**GGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTT	1225
	AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTATCC**G**GGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCT	1226
	CTATGACC**C**GGATAACA	1227
	TGTTATCC**G**GGTCATAG	1228
Cystic fibrosis Arg117Cys CGC to TGC	GTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAA**C**GCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGC	1229
	GCAGTGTCCTCACAATAAAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGC**G**TTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTAC	1230
	AGGAGGAA**C**GCTCTATC	1231
	GATAGAGC**G**TTCCTCCT	1232
Cystic fibrosis Arg117His CGC to CAC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAAC**G**CTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1233
	AGCAGTGTCCTCACAATAAAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAG**C**GTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTA	1234
	GGAGGAAC**G**CTCTATCG	1235
	CGATAGAG**C**GTTCCTCC	1236
Cystic fibrosis Arg117Leu CGC to CTC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAAC**G**CTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1237
	AGCAGTGTCCTCACAATAAAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAG**C**GTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTA	1238
	GGAGGAAC**G**CTCTATCG	1239
	CGATAGAG**C**GTTCCTCC	1240

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Arg117Pro CGC to CCC	TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAAC**G**CTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT	1241
	AGCAGTGTCCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAG**C**GTTCCTCCTTGTTATCCGGGTCA TAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTA	1242
	GGAGGAAC**G**CTCTATCG	1243
	CGATAGAG**C**GTTCCTCC	1244
Cystic fibrosis Ala120Thr GCG-ACG	CTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAAC AAGGAGGAACGCTCTATC**G**CGATTTATCTAGGCATAGGCTTA TGCCTTCTCTTTATTGTGAGGACACTGCTCCTACACC	1245
	GGTGTAGGAGCAGTGTCCTCACAATAAAGAGAAGGCATAAG CCTATGCCTAGATAAATCG**C**GATAGAGCGTTCCTCCTTGTTA TCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAG	1246
	GCTCTATC**G**CGATTTAT	1247
	ATAAATCG**C**GATAGAGC	1248
Cystic fibrosis Tyr122Term TAT to TAA	GGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGA ACGCTCTATCGCGATTTA**T**CTAGGCATAGGCTTATGCCTTCT CTTTATTGTGAGGACACTGCTCCTACACCCAGCCATT	1249
	AATGGCTGGGTGTAGGAGCAGTGTCCTCACAATAAAGAGAA GGCATAAGCCTATGCCTAG**A**TAAATCGCGATAGAGCGTTCCT CCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCC	1250
	GCGATTTA**T**CTAGGCAT	1251
	ATGCCTAG**A**TAAATCGC	1252
Cystic fibrosis Gly126Asp GGC-GAC	TAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCG CGATTTATCTAGGCATAG**G**CTTATGCCTTCTCTTTATTGTGAG GACACTGCTCCTACACCCAGCCATTTTTGGCCTTCA	1253
	TGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCCTCAC AATAAAGAGAAGGCATAAG**C**CTATGCCTAGATAAATCGCGAT AGAGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTA	1254
	AGGCATAG**G**CTTATGCC	1255
	GGCATAAG**C**CTATGCCT	1256

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis His139Arg CAC to CGC	TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGT GAGGACACTGCTCCTAC**A**CCCAGCCATTTTTGGCCTTCATCA CATTGGAATGCAGATGAGAATAGCTATGTTTAGTTT	1257
	AAACTAAACATAGCTATTCTCATCTGCATTCCAATGTGATGAA GGCCAAAAATGGCTGGG**T**GTAGGAGCAGTGTCCTCACAATA AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGA	1258
	GCTCCTAC**A**CCCAGCCA	1259
	TGGCTGGG**T**GTAGGAGC	1260
Cystic fibrosis Ala141Asp GCC to GAC	TTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGAC ACTGCTCCTACACCCAG**C**CATTTTTGGCCTTCATCACATTGG AATGCAGATGAGAATAGCTATGTTTAGTTTGATTTA	1261
	TAAATCAAACTAAACATAGCTATTCTCATCTGCATTCCAATGT GATGAAGGCCAAAAATG**G**CTGGGTGTAGGAGCAGTGTCCTC ACAATAAAGAGAAGGCATAAGCCTATGCCTAGATAAA	1262
	ACACCCAG**C**CATTTTTG	1263
	CAAAAATG**G**CTGGGTGT	1264
Cystic fibrosis Ile148Thr ATT to ACT	GCCTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCA TTTTTGGCCTTCATCACA**T**TGGAATGCAGATGAGAATAGCTAT GTTTAGTTTGATTTATAAGAAGGTAATACTTCCTTG	1265
	CAAGGAAGTATTACCTTCTTATAAATCAAACTAAACATAGCTA TTCTCATCTGCATTCCA**A**TGTGATGAAGGCCAAAAATGGCTG GGTGTAGGAGCAGTGTCCTCACAATAAAGAGAAGGC	1266
	TCATCACA**T**TGGAATGC	1267
	GCATTCCA**A**TGTGATGA	1268
Cystic fibrosis Gly149Arg GGA to AGA	CTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCATTT TTGGCCTTCATCACATT**G**GAATGCAGATGAGAATAGCTATGTT TAGTTTGATTTATAAGAAGGTAATACTTCCTTGCA	1269
	TGCAAGGAAGTATTACCTTCTTATAAATCAAACTAAACATAGC TATTCTCATCTGCATTC**C**AATGTGATGAAGGCCAAAAATGGCT GGGTGTAGGAGCAGTGTCCTCACAATAAAGAGAAG	1270
	ATCACATT**G**GAATGCAG	1271
	CTGCATTC**C**AATGTGAT	1272

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Cystic fibrosis Gln151Term CAG to TAG	TTTATTGTGAGGACACTGCTCCTACACCCAGCCATTTTTGGC CTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTT TGATTTATAAGAAGGTAATACTTCCTTGCACAGGCC	1273
	GGCCTGTGCAAGGAAGTATTACCTTCTTATAAATCAAACTAAA CATAGCTATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAA ATGGCTGGGTGTAGGAGCAGTGTCCTCACAATAAA	1274
	TTGGAATGCAGATGAGA	1275
	TCTCATCTGCATTCCAA	1276
Cystic fibrosis Lys166Glu AAG-GAG	AATATATTTGTATTTTGTTTGTTGAAATTATCTAACTTTCCATTT TTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAA TAAGTATTGGACAACTTGTTAGTCTCCTTTCCA	1277
	TGGAAAGGAGACTAACAAGTTGTCCAATACTTATTTTATCTAG AACACGGCTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA GTTAGATAATTTCAACAAACAAAATACAAATATATT	1278
	AGACTTTAAAGCTGTCA	1279
	TGACAGCTTTAAAGTCT	1280
Cystic fibrosis Ile175Val ATA-GTA	TTATCTAACTTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAG CCGTGTTCTAGATAAAATAAGTATTGGACAACTTGTTAGTCTC CTTTCCAACAACCTGAACAAATTTGATGAAGTAT	1281
	ATACTTCATCAAATTTGTTCAGGTTGTTGGAAAGGAGACTAAC AAGTTGTCCAATACTTATTTTATCTAGAACACGGCTTGACAGC TTTAAAGTCTAAAAGAAAAATGGAAAGTTAGATAA	1282
	TAGATAAAATAAGTATT	1283
	AATACTTATTTTATCTA	1284
Cystic fibrosis Gly178Arg GGA to AGA	TTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCT AGATAAAATAAGTATTGGACAACTTGTTAGTCTCCTTTCCAAC AACCTGAACAAATTTGATGAAGTATGTACCTATT	1285
	AATAGGTACATACTTCATCAAATTTGTTCAGGTTGTTGGAAAG GAGACTAACAAGTTGTCCAATACTTATTTTATCTAGAACACGG CTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA	1286
	TAAGTATTGGACAACTT	1287
	AAGTTGTCCAATACTTA	1288
Cystic fibrosis His199Gln CAT to CAG	AAGATACAATGACACCTGTTTTTGCTGTGCTTTTATTTTCCAG GGACTTGCATTGGCACATTTCGTGTGGATCGCTCCTTTGCAA GTGGCACTCCTCATGGGGCTAATCTGGGAGTTGTTA	1289

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAA AGGAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGA AAATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTT	1290
	TTGGCACATTTCGTGTG	1291
	CACACGAAATGTGCCAA	1292
Cystic fibrosis His199Tyr CAT to TAT	GGAAGATACAATGACACCTGTTTTTGCTGTGCTTTTATTTTCC AGGGACTTGCATTGGCACATTTCGTGTGGATCGCTCCTTTGC AAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTGT	1293
	ACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAG GAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGAAA ATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTTCC	1294
	CATTGGCACATTTCGTG	1295
	CACGAAATGTGCCAATG	1296
Cystic fibrosis Pro205Ser CCT to TCT	TGTTTTTGCTGTGCTTTTATTTTCCAGGGACTTGCATTGGCAC ATTTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGG GGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCT	1297
	AGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCATG AGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAATGTGC CAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAAAACA	1298
	GGATCGCTCCTTTGCAA	1299
	TTGCAAAGGAGCGATCC	1300
Cystic fibrosis Leu206Trp TTG to TGG	TTTGCTGTGCTTTTATTTTCCAGGGACTTGCATTGGCACATTT CGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGGC TAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGG	1301
	CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAAT GTGCCAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAA	1302
	CGCTCCTTTGCAAGTGG	1303
	CCACTTGCAAAGGAGCG	1304
Cystic fibrosis Gln220Term CAG to TAG	TTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGG GCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGGACT TGGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGGC	1305
	GCCCAGCCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGT CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAA	1306

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGTTGTTACAGGCGTCT	1307
	AGACGCCTGTAACAACT	1308
Cystic fibrosis Cys225Arg TGT-CGT	CCTTTGCAAGTGGCACTCCTCATGGGGCTAATCTGGGAGTT GTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTCAGGCTGGGCTAGGGAGAATGATGA	1309
	TCATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTA TCAGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAACAAC TCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAGG	1310
	CTGCCTTCTGTGGACTT	1311
	AAGTCCACAGAAGGCAG	1312
Cystic fibrosis Val232Asp GTC to GAC	TGGGGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGT GGACTTGGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGG CTAGGGAGAATGATGATGAAGTACAGGTAGCAACCTAT	1313
	ATAGGTTGCTACCTGTACTTCATCATCATTCTCCCTAGCCCA GCCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGTCCACA GAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCA	1314
	CCTGATAGTCCTTGCCC	1315
	GGGCAAGGACTATCAGG	1316
Cystic fibrosis Gly239Arg GGG to AGG	GTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTCAGGCTGGGCTAGGGAGAATGATGATGAA GTACAGGTAGCAACCTATTTTCATAACTTGAAAGTTT	1317
	AAACTTTCAAGTTATGAAAATAGGTTGCTACCTGTACTTCATC ATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTATC AGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAAC	1318
	TTTCAGGCTGGGCTAGG	1319
	CCTAGCCCAGCCTGAAA	1320

EXAMPLE 10
Cyclin-dependent kinase inhibitor 2A - CDKN2A

The human CDKN2A gene was also designated MTS-1 for multiple tumor suppressor-1 and has been implicated in multiple cancers including, for example, malignant melanoma. Malignant melanoma is a cutaneous neoplasm of melanocytes. Melanomas generally have features of asymmetry, irregular border, variegated color, and diameter greater than 6 mm. The precise cause of melanoma is

unknown, but sunlight and heredity are risk factors. Melanoma has been increasing during the past few decades.

The CDKN2A gene has been found to be homozygously deleted at high frequency in cell lines derived from tumors of lung, breast, brain, bone, skin, bladder, kidney, ovary, and lymphocyte. Melanoma cell lines carried at least one copy of CDKN2A in combination with a deleted allele. Melanoma cell lines that carried at least 1 copy of CDKN2A frequently showed nonsense, missense, or frameshift mutations in the gene. Thus, CDKN2A may rival p53 (see Example 5) in the universality of its involvement in tumorigenesis. The attached table discloses the correcting oligonucleotide base sequences for the CDKN2A oligonucleotides of the invention.

Table 17
CDKN2A Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Melanoma Trp15Term TGG-TAG	GGGCGGCGGGGAGCAGCATGGAGCCGGCGGCGGGGAGCAG CATGGAGCCTTCGGCTGACT**G**GCTGGCCACGGCCGCGGCCC GGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGG	1321
	CCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACCCCG GGCCGCGGCCGTGGCCAGC**C**AGTCAGCCGAAGGCTCCATGC TGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCGCCC	1322
	GGCTGACT**G**GCTGGCCA	1323
	TGGCCAGC**C**AGTCAGCC	1324
Melanoma Leu16Pro CTG-CCG	CGGCGGGGAGCAGCATGGAGCCGGCGGCGGGGAGCAGCAT GGAGCCTTCGGCTGACTGGC**T**GGCCACGGCCGCGGCCCGG GGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGG C	1325
	GCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACC CCGGGCCGCGGCCGTGGCC**A**GCCAGTCAGCCGAAGGCTCC ATGCTGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCG	1326
	TGACTGGC**T**GGCCACGG	1327
	CCGTGGCC**A**GCCAGTCA	1328
Melanoma Gly23Asp GGT-GAT	CGGCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTG GCCACGGCCGCGGCCCGGG**G**TCGGGTAGAGGAGGTGCGGG CGCTGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAG	1329
	CTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGCGC CCGCACCTCCTCTACCCGA**C**CCCGGGCCGCGGCCGTGGCCA GCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGCCG	1330
	GGCCCGGG**G**TCGGGTAG	1331

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTACCCGA**C**CCCGGGCC	1332
Melanoma Arg24Pro CGG-CCG	CGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC ACGGCCGCGGCCCGGGGTC**G**GGTAGAGGAGGTGCGGGCGC TGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAGTTA	1333
	TAACTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGC GCCCGCACCTCCTCTACC**C**GACCCCGGGCCGCGGCCGTGGC CAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCG	1334
	CCGGGGTC**G**GGTAGAGG	1335
	CCTCTACC**C**GACCCCGG	1336
Melanoma Leu32Pro CTG-CCG	CGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCGGGT AGAGGAGGTGCGGGCGCTGC**T**GGAGGCGGGGGCGCTGCCC AACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTGGG	1337
	CCCACCTGGATCGGCCTCCGACCGTAACTATTCGGTGCGTTG GGCAGCGCCCCCGCCTCC**A**GCAGCGCCCGCACCTCCTCTAC CCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCG	1338
	GGCGCTGC**T**GGAGGCGG	1339
	CCGCCTCC**A**GCAGCGCC	1340
Melanoma Gly35Ala GGG-GCG	GGCTGGCCACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGT GCGGGCGCTGCTGGAGGCGG**G**GGCGCTGCCCAACGCACCG AATAGTTACGGTCGGAGGCCGATCCAGGTGGGTAGAGGGTC	1341
	GACCCTCTACCCACCTGGATCGGCCTCCGACCGTAACTATTC GGTGCGTTGGGCAGCGCC**C**CCCGCCTCCAGCAGCGCCCGCAC CTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCC	1342
	GGAGGCGG**G**GGCGCTGC	1343
	GCAGCGCC**C**CCGCCTCC	1344
Melanoma Tyr44Term TACg-TAA	GGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTG CCCAACGCACCGAATAGTTA**C**GGTCGGAGGCCGATCCAGGTG GGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGA	1345
	TCGCCCGCCATCCCCTGCTCCCGCTGCAGACCCTCTACCCAC CTGGATCGGCCTCCGACC**G**TAACTATTCGGTGCGTTGGGCAG CGCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACC	1346
	AATAGTTA**C**GGTCGGAG	1347
	CTCCGACC**G**TAACTATT	1348
Melanoma Met53Ile ATGa-ATC	TCTCCCATACCTGCCCCCACCCTGGCTCTGACCACTCTGCTC TCTCTGGCAGGTCATGAT**G**ATGGGCAGCGCCCGCGTGGCGG AGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCA	1349
	TGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCG CCACGCGGGCGCTGCCCAT**C**ATCATGACCTGCCAGAGAGAG CAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGGAGA	1350
	GTCATGAT**G**ATGGGCAG	1351

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGCCCAT**C**ATCATGAC	1352
Melanoma Met54Ile ATGg-ATT	CCCATACCTGCCCCCACCCTGGCTCTGACCACTCTGCTCTCT CTGGCAGGTCATGATGAT**G**GGCAGCGCCCGCGTGGCGGAGC TGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCAGAC	1353
	GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCC**C**ATCATCATGACCTGCCAGAGA GAGCAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGG	1354
	ATGATGAT**G**GGCAGCGC	1355
	GCGCTGCC**C**ATCATCAT	1356
Melanoma Ser56Ile AGC-ATC	GCCGGCCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGC AGGTCATGATGATGGGCA**G**CGCCCGAGTGGCGGAGCTGCTG CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGC	1357
	GCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCA GCAGCTCCGCCACTCGGGCG**C**TGCCCATCATCATGACCTGCC AGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCCGGC	1358
	GATGGGCA**G**CGCCCGAG	1359
	CTCGGGCG**C**TGCCCATC	1360
Melanoma Ala57Val GCC-GTC	GGCCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGG TCATGATGATGGGCAGCG**C**CCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC	1361
	GTGGCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGG**G**CGCTGCCCATCATCATGACCT GCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCC	1362
	GGGCAGCG**C**CCGAGTGG	1363
	CCACTCGG**G**CGCTGCCC	1364
Melanoma Arg58Term cCGA-TGA	CCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTC ATGATGATGGGCAGCGCC**C**GAGTGGCGGAGCTGCTGCTGCT CCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTC	1365
	GAGTGGCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTC**G**GGCGCTGCCCATCATCATGAC CTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGG	1366
	GCAGCGCC**C**GAGTGGCG	1367
	CGCCACTC**G**GGCGCTGC	1368
Melanoma Val59Gly GTG-GGG	CACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGAT GATGGGCAGCGCCCGAG**T**GGCGGAGCTGCTGCTGCTCCACG GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCAC	1369
	GTGAGAGTGGCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTG GAGCAGCAGCAGCTCCGCC**A**CTCGGGCGCTGCCCATCATCA TGACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTG	1370
	CGCCCGAG**T**GGCGGAGC	1371

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCTCCGCC**A**CTCGGGCG	1372
Melanoma Leu62Pro CTG-CCG	TCTGACCACTCTGCTCTCTCTGGCAGGTCATGATGATGGGCA GCGCCCGCGTGGCGGAGC**T**GCTGCTGCTCCACGGCGCGGA GCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGT	1373
	ACCGGTCGGGTGAGAGTGGCAGGGTCTGCGCAGTTGGGCTC CGCGCCGTGGAGCAGCAGC**A**GCTCCGCCACGCGGGCGCTG CCCATCATCATGACCTGCCAGAGAGAGCAGAGTGGTCAGA	1374
	GGCGGAGC**T**GCTGCTGC	1375
	GCAGCAGC**A**GCTCCGCC	1376
Melanoma Ala68Val GCG-GTG	TCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAG CTGCTGCTGCTCCACGGCG**C**GGAGCCCAACTGCGCAGACCC TGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGA	1377
	TCCCGGGCAGCATCATGCACCGGTCGGGTGAGAGTGGCAGG GTCTGCGCAGTTGGGCTCC**G**CGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCCATCATCATGACCTGCCAGA	1378
	CCACGGCG**C**GGAGCCCA	1379
	TGGGCTCC**G**CGCCGTGG	1380
Melanoma Asn71Lys AACt-AAA	CATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGC TCCACGGCGCGGAGCCCAA**C**TGCGCCGACCCCGCCACTCTC ACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTG	1381
	CAGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCGGGTGA GAGTGGCGGGGTCGGCGCA**G**TTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATG	1382
	GAGCCCAA**C**TGCGCCGA	1383
	TCGGCGCA**G**TTGGGCTC	1384
Melanoma Asn71Ser AAC-AGC	TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCA**A**CTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCT	1385
	AGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCGGGTGAG AGTGGCGGGGTCGGCGCAG**T**TGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGA	1386
	GGAGCCCA**A**CTGCGCCG	1387
	CGGCGCAG**T**TGGGCTCC	1388
Melanoma Pro81Leu CCC-CTC	AGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGAC CCCGCCACTCTCACCCGAC**C**CGTGCACGACGCTGCCCGGGA GGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGG	1389
	CCGGCCCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTC CCGGGCAGCGTCGTGCACG**G**GTCGGGTGAGAGTGGCGGGG TCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT	1390
	CACCCGAC**C**CGTGCACG	1391

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGTGCACG**G**GTCGGGTG	1392
Melanoma Asp84Tyr cGAC-TAC	CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC TCTCACCCGACCCGTGCAC**G**ACGCTGCCCGGGAGGGCTTCC TGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGC	1393
	GCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCCAGG AAGCCCTCCCGGGCAGCGT**C**GTGCACGGGTCGGGTGAGAGT GGCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAG	1394
	CCGTGCAC**G**ACGCTGCC	1395
	GGCAGCGT**C**GTGCACGG	1396
Melanoma Ala85Thr cGCT-ACT	CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGAC**G**CTGCCCGGGAGGGCTTCCTGG ACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGCTGG	1397
	CCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCC AGGAAGCCCTCCCGGGCAG**C**GTCGTGCACGGGTCGGGTGAG AGTGGCGGGGTCGGCGCAGTTGGGCTCCGCGCCGTGGAG	1398
	TGCACGAC**G**CTGCCCGG	1399
	CCGGGCAG**C**GTCGTGCA	1400
Melanoma Arg87Pro CGG-CCG	GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA CCCGTGCACGACGCTGCCC**G**GGAGGGCTTCCTGGACACGCT GGTGGTGCTGCACCGGGCCGGGGCGCGGCTGGACGTGCG	1401
	CGCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCC**C**GGGCAGCGTCGTGCACGGGTC GGGTGAGAGTGGCGGGGTCGGCGCAGTTGGGCTCCGCGC	1402
	CGCTGCCC**G**GGAGGGCT	1403
	AGCCCTCC**C**GGGCAGCG	1404
Melanoma Arg87Trp cCGG-TGG	GGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCG ACCCGTGCACGACGCTGCC**C**GGGAGGGCTTCCTGGACACGC TGGTGGTGCTGCACCGGGCCGGGGCGCGGCTGGACGTGC	1405
	GCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGC GTGTCCAGGAAGCCCTCCC**G**GGCAGCGTCGTGCACGGGTCG GGTGAGAGTGGCGGGGTCGGCGCAGTTGGGCTCCGCGCC	1406
	ACGCTGCC**C**GGGAGGGC	1407
	GCCCTCCC**G**GGCAGCGT	1408
Melanoma Leu97Arg CTG-CGG	CTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTC CTGGACACGCTGGTGGTGC**T**GCACCGGGCCGGGGCGCGGCT GGACGTGCGCGATGCCTGGGGTCGTCTGCCCGTGGACTT	1409
	AAGTCCACGGGCAGACGACCCCAGGCATCGCGCACGTCCAG CCGCGCCCCGGCCCGGTGC**A**GCACCACCAGCGTGTCCAGGA AGCCCTCCCGGGCAGCATCATGCACCGGTCGGGTGAGAG	1410
	GGTGGTGC**T**GCACCGGG	1411

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCCGGTGC**A**GCACCACC	1412
Melanoma Arg99Pro CGG-CCG	CCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGAC ACGCTGGTGGTGCTGCACC**G**GGCCGGGGCGCGGCTGGACG TGCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGA	1413
	TCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCGCGCAC GTCCAGCCGCGCCCCGGCC**C**GGTGCAGCACCACCAGCGTGT CCAGGAAGCCCTCCCGGGCAGCATCATGCACCGGTCGGG	1414
	GCTGCACC**G**GGCCGGGG	1415
	CCCCGGCC**C**GGTGCAGC	1416
Melanoma Gly101Trp cGGG-TGG	CCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGACACGCT GGTGGTGCTGCACCGGGCC**G**GGGCGCGGCTGGACGTGCGC GATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGC	1417
	GCTCCTCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCG CGCACGTCCAGCCGCGCCC**C**GGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCCCGGGCAGCATCATGCACCGG	1418
	ACCGGGCC**G**GGGCGCGG	1419
	CCGCGCCC**C**GGCCCGGT	1420
Melanoma Arg107Cys gCGC-TGC	CGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGC CGGGGCGCGGCTGGACGTG**C**GCGATGCCTGGGGTCGTCTGC CCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTG	1421
	CAACGTCGCGGTGGCCCCGCTCCTCGGCCAAGTCCACGGGC AGACGACCCCAGGCATCGC**G**CACGTCCAGCCGCGCCCCGGC CCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTCCCG	1422
	TGGACGTG**C**GCGATGCC	1423
	GGCATCGC**G**CACGTCCA	1424
Melanoma Ala118Thr gGCT-ACT	CACCGGGCCGGGGCGCGGCTGGACGTGCGCGATGCCTGGG GCCGTCTGCCCGTGGACCTG**G**CTGAGGAGCTGGGCCATCGC GATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGGCACCA	1425
	TGGTGCCCCCCGCAGCCGCGCGCAGGTACCGTGCGACATCG CGATGGCCCAGCTCCTCAG**C**CAGGTCCACGGGCAGACGGCC CCAGGCATCGCGCACGTCCAGCCGCGCCCCGGCCCGGTG	1426
	TGGACCTG**G**CTGAGGAG	1427
	CTCCTCAG**C**CAGGTCCA	1428
Melanoma Val126Asp GTC-GAC	TGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAG GAGCTGGGCCATCGCGATG**T**CGCACGGTACCTGCGCGCGGC TGCGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGA	1429
	TCTATGCGGGCATGGTTACTGCCTCTGGTGCCCCCCGCAGCC GCGCGCAGGTACCGTGCG**A**CATCGCGATGGCCCAGCTCCTC AGCCAGGTCCACGGGCAGACGGCCCCAGGCATCGCGCA	1430
	TCGCGATG**T**CGCACGGT	1431

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACCGTGCGACATCGCGA	1432

EXAMPLE 11
Adenomatous polyposis of the colon - APC

Adenomatous polyposis of the colon is characterized by adenomatous polyps of the colon and rectum; in extreme cases the bowel is carpeted with a myriad of polyps. This is a viciously premalignant disease with one or more polyps progressing through dysplasia to malignancy in untreated gene carriers with a median age at diagnosis of 40 years.

Mutations in the APC gene are an initiating event for both familial and sporadic colorectal tumorigenesis and many alleles of the APC gene have been identified. Carcinoma may arise at any age from late childhood through the seventh decade with presenting features including, for example, weight loss and inanition, bowel obstruction, or bloody diarrhea. Cases of new mutation still present in these ways but in areas with well organized registers most other gene carriers are detected. The attached table discloses the correcting oligonucleotide base sequences for the APC oligonucleotides of the invention.

Table 18
APC Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Arg121Term AGA-TGA	GGATCTGTATCAAGCCGTTCTGGAGAGTGCAGTCCTGTTCCT ATGGGTTCATTTCCAAGA**A**GAGGGTTTGTAAATGGAAGCAGA GAAAGTACTGGATATTTAGAAGAACTTGAGAAAGAGA	1433
	TCTCTTTCTCAAGTTCTTCTAAATATCCAGTACTTTCTCTGCTT CCATTTACAAACCCTC**T**TCTTGGAAATGAACCCATAGGAACAG GACTGCACTCTCCAGAACGGCTTGATACAGATCC	1434
	TTCCAAGA**A**GAGGGTTT	1435
	AAACCCTC**T**TCTTGGAA	1436
Adenomatous polyposis coli Trp157Term TGG-TAG	AAAAAAAAAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAA GAAAAGGAAAAAGACT**G**GTATTACGCTCAACTTCAGAATCTCA CTAAAAGAATAGATAGTCTTCCTTTAACTGAAAA	1437
	TTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTG AAGTTGAGCGTAATAC**C**AGTCTTTTTCCTTTTCTTCTTTGTCAA GATCAGCAAGAAGCAATGACCTATTTTTTTTTT	1438
	AAAAGACT**G**GTATTACG	1439
	CGTAATAC**C**AGTCTTTT	1440
Adenomatous polyposis coli Tyr159Term TAC-TAG	AAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAG GAAAAAGACTGGTATTA**C**GCTCAACTTCAGAATCTCACTAAAA GAATAGATAGTCTTCCTTTAACTGAAAATGTAAGT	1441
	ACTTACATTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGA GATTCTGAAGTTGAGC**G**TAATACCAGTCTTTTTCCTTTTCTTCT TTGTCAAGATCAGCAAGAAGCAATGACCTATTT	1442
	TGGTATTA**C**GCTCAACT	1443
	AGTTGAGC**G**TAATACCA	1444
Adenomatous polyposis coli Gln163Term CAG-TAG	TTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAAGACT GGTATTACGCTCAACTT**C**AGAATCTCACTAAAAGAATAGATAG TCTTCCTTTAACTGAAAATGTAAGTAACTGGCAGT	1445
	ACTGCCAGTTACTTACATTTTCAGTTAAAGGAAGACTATCTATT CTTTTAGTGAGATTCT**G**AAGTTGAGCGTAATACCAGTCTTTTTC CTTTTCTTCTTTGTCAAGATCAGCAAGAAGCAA	1446
	CTCAACTT**C**AGAATCTC	1447
	GAGATTCT**G**AAGTTGAG	1448
Adenomatous polyposis coli Arg168Term AGA-TGA	CTTGACAAAGAAGAAAAGGAAAAAGACTGGTATTACGCTCAAC TTCAGAATCTCACTAAA**A**GAATAGATAGTCTTCCTTTAACTGAA AATGTAAGTAACTGGCAGTACAACTTATTTGAAA	1449
	TTTCAAATAAGTTGTACTGCCAGTTACTTACATTTTCAGTTAAA GGAAGACTATCTATTC**T**TTTAGTGAGATTCTGAAGTTGAGCGT AATACCAGTCTTTTTCCTTTTCTTCTTTGTCAAG	1450

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCACTAAA**A**GAATAGAT	1451
	ATCTATTC**T**TTTAGTGA	1452
Adenomatous polyposis coli Ser171Ile AGT-ATT	AAGAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCT CACTAAAAGAATAGATA**G**TCTTCCTTTAACTGAAAATGTAAGTA ACTGGCAGTACAACTTATTTGAAACTTTAATAAC	1453
	GTTATTAAAGTTTCAAATAAGTTGTACTGCCAGTTACTTACATT TTCAGTTAAAGGAAGA**C**TATCTATTCTTTTAGTGAGATTCTGAA GTTGAGCGTAATACCAGTCTTTTTCCTTTTCTT	1454
	AATAGATA**G**TCTTCCTT	1455
	AAGGAAGA**C**TATCTATT	1456
Adenomatous polyposis coli Gln181Term CAA-TAA	GATTAACGTAAATACAAGATATTGATACTTTTTTATTATTTGTGG TTTTAGTTTTCCTTA**C**AAACAGATATGACCAGAAGGCAATTGG AATATGAAGCAAGGCAAATCAGAGTTGCGATGG	1457
	CCATCGCAACTCTGATTTGCCTTGCTTCATATTCCAATTGCCT TCTGGTCATATCTGTTT**G**TAAGGAAAACTAAAACCACAAATAAT AAAAAAGTATCAATATCTTGTATTTACGTTAATC	1458
	TTTCCTTA**C**AAACAGAT	1459
	ATCTGTTT**G**TAAGGAAA	1460
Adenomatous polyposis coli Glu190Term GAA-TAA	CTTTTTTATTATTTGTGGTTTTAGTTTTCCTTACAAACAGATATG ACCAGAAGGCAATTG**G**AATATGAAGCAAGGCAAATCAGAGTT GCGATGGAAGAACAACTAGGTACCTGCCAGGATA	1461
	TATCCTGGCAGGTACCTAGTTGTTCTTCCATCGCAACTCTGAT TTGCCTTGCTTCATATT**C**CAATTGCCTTCTGGTCATATCTGTTT GTAAGGAAAACTAAAACCACAAATAATAAAAAAG	1462
	GGCAATTG**G**AATATGAA	1463
	TTCATATT**C**CAATTGCC	1464
Adenomatous polyposis coli Gln208Term CAG-TAG	CAATTGGAATATGAAGCAAGGCAAATCAGAGTTGCGATGGAA GAACAACTAGGTACCTGC**C**AGGATATGGAAAAACGAGCACAG GTAAGTTACTTGTTTCTAAGTGATAAAACAGCGAAGA	1465
	TCTTCGCTGTTTTATCACTTAGAAACAAGTAACTTACCTGTGCT CGTTTTTCCATATCCT**G**GCAGGTACCTAGTTGTTCTTCCATCG CAACTCTGATTTGCCTTGCTTCATATTCCAATTG	1466
	GTACCTGC**C**AGGATATG	1467
	CATATCCT**G**GCAGGTAC	1468
Adenomatous polyposis coli Arg213Term CGA-TGA	GCAAGGCAAATCAGAGTTGCGATGGAAGAACAACTAGGTACC TGCCAGGATATGGAAAAA**C**GAGCACAGGTAAGTTACTTGTTTC TAAGTGATAAAACAGCGAAGAGCTATTAGGAATAAA	1469
	TTTATTCCTAATAGCTCTTCGCTGTTTTATCACTTAGAAACAAG TAACTTACCTGTGCTC**G**TTTTTCCATATCCTGGCAGGTACCTA GTTGTTCTTCCATCGCAACTCTGATTTGCCTTGC	1470
	TGGAAAAA**C**GAGCACAG	1471
	CTGTGCTC**G**TTTTTCCA	1472

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Arg232Term CGA-TGA	GTTTTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAAAGGACATACTTCGTATA**C**GACAGCTTTTACAGTCCCAAGCAACAGAAGCAGAGGTTAGTAAATTGCCTTTCTTGTTTG	1473
	CAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGCTTGGGACTGTAAAAGCTGTC**G**TATACGAAGTATGTCCTTTTCGATTTGCTGAATTCTGGCTATTCTTCGCTAAAATAAAAC	1474
	TTCGTATA**C**GACAGCTT	1475
	AAGCTGTC**G**TATACGAA	1476
Adenomatous polyposis coli Gln233Term CAG-TAG	TTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAAAGGACATACTTCGTATACGA**C**AGCTTTTACAGTCCCAAGCAACAGAAGCAGAGGTTAGTAAATTGCCTTTCTTGTTTGTGG	1477
	CCACAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGCTTGGGACTGTAAAAGCT**G**TCGTATACGAAGTATGTCCTTTTCGATTTGCTGAATTCTGGCTATTCTTCGCTAAAATAA	1478
	GTATACGA**C**AGCTTTTA	1479
	TAAAAGCT**G**TCGTATAC	1480
Adenomatous polyposis coli Gln247Term CAG-TAG	AGAAAGCCTACACCATTTTTGCATGTACTGATGTTAACTCCATCTTAACAGAGGTCATCT**C**AGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAGAATGAAGGTCAAGGAGTGG	1481
	CCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGGTTTCATGCTTGTTCT**G**AGATGACCTCTGTTAAGATGGAGTTAACATCAGTACATGCAAAAATGGTGTAGGCTTTCT	1482
	GGTCATCT**C**AGAACAAG	1483
	CTTGTTCT**G**AGATGACC	1484
Adenomatous polyposis coli Gly267Term GGA-TGA	CAGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAGAATGAAGGTCAAGGAGTG**G**GAGAAATCAACATGGCAACTTCTGGTAATGGTCAGGTAAATAAATTATTTTATCATATTT	1485
	AAATATGATAAAATAATTTATTTACCTGACCATTACCAGAAGTTGCCATGTTGATTTCTC**C**CACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGGTTTCATGCTTGTTCTG	1486
	AAGGAGTG**G**GAGAAATC	1487
	GATTTCTC**C**CACTCCTT	1488
Adenomatous polyposis coli Glu443Term GAA-TAA	CTTCAAATAACAAAGCATTATGGTTTATGTTGATTTTATTTTTCAGTGCCAGCTCCTGTT**G**AACATCAGATCTGTCCTGCTGTGTGTTCTAATGAAACTTTCATTTGATGAAGAGCATA	1489
	TATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTT**C**AACAGGAGCTGGCACTGAAAAATAAAATCAACATAAACCATAATGCTTTGTTATTTGAAG	1490
	CTCCTGTT**G**AACATCAG	1491
	CTGATGTT**C**AACAGGAG	1492
Adenomatous polyposis coli SER457TER TCA-TAA	CAGTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGTGTTCTAATGAAACTTT**C**ATTTGATGAAGAGCATAGACATGCAATGAATGAACTAGGTAAGACAAAAATGTTTTTTAA	1493

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTAAAAAACATTTTTGTCTTACCTAGTTCATTCATTGCATGTCTATGCTCTTCATCAAAT**G**AAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTTCAACAGGAGCTGGCACTG	1494
	GAAACTTT**C**ATTTGATG	1495
	CATCAAAT**G**AAAGTTTC	1496
Adenomatous polyposis *coli* Gln473Term CAG-TAG	AGTTGTTTTATTTTAGATGATTGTCTTTTTCCTCTTGCCCTTTTTAAATTAGGGGGACTA**C**AGGCCATTGCAGAATTATTGCAAGTGGACTGTGAAATGTACGGGCTTACTAATGACCACT	1497
	AGTGGTCATTAGTAAGCCCGTACATTTCACAGTCCACTTGCAATAATTCTGCAATGGCCT**G**TAGTCCCCCTAATTTAAAAAGGGCAAGAGGAAAAAGACAATCATCTAAAATAAAACAACT	1498
	GGGGACTA**C**AGGCCATT	1499
	AATGGCCT**G**TAGTCCCC	1500
Adenomatous polyposis coli Tyr486Term TAC-TAG	TTTTAAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAAGTGGACTGTGAAATGTA**C**GGGCTTACTAATGACCACTACAGTATTACACTAAGACGATATGCTGGAATGGCTTTGACA	1501
	TGTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGTGGTCATTAGTAAGCCC**G**TACATTTCACAGTCCACTTGCAATAATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAA	1502
	GAAATGTA**C**GGGCTTAC	1503
	GTAAGCCC**G**TACATTTC	1504
Adenomatous polyposis coli Arg499Term CGA-TGA	TTGCAAGTGGACTGTGAAATGTATGGGCTTACTAATGACCACTACAGTATTACACTAAGA**C**GATATGCTGGAATGGCTTTGACAAACTTGACTTTTGGAGATGTAGCCAACAAGGTATGTT	1505
	AACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTTGTCAAAGCCATTCCAGCATATC**G**TCTTAGTGTAATACTGTAGTGGTCATTAGTAAGCCCATACATTTCACAGTCCACTTGCAA	1506
	CACTAAGA**C**GATATGCT	1507
	AGCATATC**G**TCTTAGTG	1508
Adenomatous polyposis coli Tyr500Term TAT-TAG	AGTGGACTGTGAAATGTATGGGCTTACTAATGACCACTACAGTATTACACTAAGACGATA**T**GCTGGAATGGCTTTGACAAACTTGACTTTTGGAGATGTAGCCAACAAGGTATGTTTTTAT	1509
	ATAAAAACATACCTTGTTGGCTACATCTCCAAAAGTCAAGTTTGTCAAAGCCATTCCAGC**A**TATCGTCTTAGTGTAATACTGTAGTGGTCATTAGTAAGCCCATACATTTCACAGTCCACT	1510
	AGACGATA**T**GCTGGAAT	1511
	ATTCCAGC**A**TATCGTCT	1512
Adenomatous polyposis coli Lys586Term AAA-TAA	GACAAATTCCAACTCTAATTAGATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTC**A**AAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGAATAAAGCTGATA	1513
	TATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTT**T**GAGGGTTGATTCCTAGTAAGAAACAGAATATGGGTCATCTAATTAGAGTTGGAATTTGTC	1514
	CAACCCTC**A**AAAGCGTA	1515

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TACGCTTTTGAGGGTTG	1516
Adenomatous polyposis coli Leu592Term TTA-TGA	TAGATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGAATAAAGCTGATATATGTGCTGTAGATGGTGC	1517
	GCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGTTGATTCCTAGTAAGAAACAGAATATGGGTCATCTA	1518
	GAGTGCCTTATGGAATT	1519
	AATTCCATAAGGCACTC	1520
Adenomatous polyposis coli Trp593Term TGG-TAG	ATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGAATAAAGCTGATATATGTGCTGTAGATGGTGCACT	1521
	AGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGTTGATTCCTAGTAAGAAACAGAATATGGGTCAT	1522
	TGCCTTATGGAATTTGT	1523
	ACAAATTCCATAAGGCA	1524
Adenomatous polyposis coli Trp593Term TGG-TGA	TGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGAATAAAGCTGATATATGTGCTGTAGATGGTGCACTT	1525
	AAGTGCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGTTGATTCCTAGTAAGAAACAGAATATGGGTCA	1526
	GCCTTATGGAATTTGTC	1527
	GACAAATTCCATAAGGC	1528
Adenomatous polyposis coli Tyr622Term TAC-TAA	TAAAGCTGATATATGTGCTGTAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTG	1529
	CACATTCCGTAATATCCCACCTCCACTTTCAATAATGGCTAAAGTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAACCAAAAATGCAAGTGCACCATCTACAGCACATATATCAGCTTTA	1530
	CTTACTTACCGGAGCCA	1531
	TGGCTCCGGTAAGTAAG	1532
Adenomatous polyposis coli Gln625Term CAG-TAG	GATATATGTGCTGTAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTGTCCAGCT	1533
	AGCTGGACACATTCCGTAATATCCCACCTCCACTTTCAATAATGGCTAAAGTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAACCAAAAATGCAAGTGCACCATCTACAGCACATATATC	1534
	ACCGGAGCCAGACAAAC	1535
	GTTTGTCTGGCTCCGGT	1536

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Leu629Term TTA-TAA	TAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCG GAGCCAGACAAACACTT**T**AGCCATTATTGAAAGTGGAGGTGG GATATTACGGAATGTGTCCAGCTTGATAGCTACAAA	1537
	TTTGTAGCTATCAAGCTGGACACATTCCGTAATATCCCACCTC CACTTTCAATAATGGCT**A**AAGTGTTTGTCTGGCTCCGGTAAGT AAGAGTGCCAACCAAAAATGCAAGTGCACCATCTA	1538
	AAACACTT**T**AGCCATTA	1539
	TAATGGCT**A**AAGTGTTT	1540
Adenomatous polyposis coli Glu650Term GAG-TAG	GCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTGTCC AGCTTGATAGCTACAAAT**G**AGGACCACAGGTATATATAGAGTT TTATATTACTTTTAAAGTACAGAATTCATACTCTCA	1541
	TGAGAGTATGAATTCTGTACTTTAAAAGTAATATAAAACTCTAT ATATACCTGTGGTCCT**C**ATTTGTAGCTATCAAGCTGGACACAT TCCGTAATATCCCACCTCCACTTTCAATAATGGC	1542
	CTACAAAT**G**AGGACCAC	1543
	GTGGTCCT**C**ATTTGTAG	1544
Adenomatous polyposis coli Trp699Term TGG-TGA	TGCATGTGGAACTTTGTGGAATCTCTCAGCAAGAAATCCTAAA GACCAGGAAGCATTATG**G**GACATGGGGGCAGTTAGCATGCTC AAGAACCTCATTCATTCAAAGCACAAAATGATTGCT	1545
	AGCAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATG CTAACTGCCCCCATGTC**C**CATAATGCTTCCTGGTCTTTAGGAT TTCTTGCTGAGAGATTCCACAAAGTTCCACATGCA	1546
	GCATTATG**G**GACATGGG	1547
	CCCATGTC**C**CATAATGC	1548
Adenomatous polyposis coli Ser713Term TCA-TGA	AAGACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGC TCAAGAACCTCATTCATT**C**AAAGCACAAAATGATTGCTATGGG AAGTGCTGCAGCTTTAAGGAATCTCATGGCAAATAG	1549
	CTATTTGCCATGAGATTCCTTAAAGCTGCAGCACTTCCCATAG CAATCATTTTGTGCTTT**G**AATGAATGAGGTTCTTGAGCATGCT AACTGCCCCCATGTCCCATAATGCTTCCTGGTCTT	1550
	CATTCATT**C**AAAGCACA	1551
	TGTGCTTT**G**AATGAATG	1552
Adenomatous polyposis coli Ser722Gly AGT-GGT	GGGGCAGTTAGCATGCTCAAGAACCTCATTCATTCAAAGCAC AAAATGATTGCTATGGGA**A**GTGCTGCAGCTTTAAGGAATCTCA TGGCAAATAGGCCTGCGAAGTACAAGGATGCCAATA	1553
	TATTGGCATCCTTGTACTTCGCAGGCCTATTTGCCATGAGATT CCTTAAAGCTGCAGCAC**T**TCCCATAGCAATCATTTTGTGCTTT GAATGAATGAGGTTCTTGAGCATGCTAACTGCCCC	1554
	CTATGGGA**A**GTGCTGCA	1555
	TGCAGCAC**T**TCCCATAG	1556

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Leu764Term TTA-TAA	TCTCCTGGCTCAGCTTGCCATCTCTTCATGTTAGGAAACAAAA AGCCCTAGAAGCAGAAT**T**AGATGCTCAGCACTTATCAGAAACT TTTGACAATATAGACAATTTAAGTCCCAAGGCATC	1557
	GATGCCTTGGGACTTAAATTGTCTATATTGTCAAAAGTTTCTGA TAAGTGCTGAGCATCT**A**ATTCTGCTTCTAGGGCTTTTTGTTTC CTAACATGAAGAGATGGCAAGCTGAGCCAGGAGA	1558
	AGCAGAAT**T**AGATGCTC	1559
	GAGCATCT**A**ATTCTGCT	1560
Adenomatous polyposis coli Ser784Thr TCT-ACT	TTAGATGCTCAGCACTTATCAGAAACTTTTGACAATATAGACAA TTTAAGTCCCAAGGCA**T**CTCATCGTAGTAAGCAGAGACACAG CAAGTCTCTATGGTGATTATGTTTTTGACACCATC	1561
	GATGGTGTCAAAAACATAATCACCATAGAGACTTGCTGTGTCT CTGCTTACTACGATGAG**A**TGCCTTGGGACTTAAATTGTCTATA TTGTCAAAAGTTTCTGATAAGTGCTGAGCATCTAA	1562
	CCAAGGCA**T**CTCATCGT	1563
	ACGATGAG**A**TGCCTTGG	1564
Adenomatous polyposis coli Arg805Term CGA-TGA	CTCATCGTAGTAAGCAGAGACACAGCAAGTCTCTATGGTGATT ATGTTTTTGACACCAAT**C**GACATGATGATAATAGGTCAGACAT TTTAATACTGGCACATGACTGTCCTTTCACCATAT	1565
	ATATGGTGAAAGGACAGTCATGTGCCAGTATTAAAATGTCTGA CCTATTATCATCATGTC**G**ATTGGTGTCAAAAACATAATCACCAT AGAGACTTGCTGTGTCTCTGCTTACTACGATGAG	1566
	ACACCAAT**C**GACATGAT	1567
	ATCATGTC**G**ATTGGTGT	1568
Adenomatous polyposis coli Gln879Term CAG-TAG	GGTCTAGGCAACTACCATCCAGCAACAGAAAATCCAGGAACT TCTTCAAAGCGAGGTTTG**C**AGATCTCCACCACTGCAGCCCAG ATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTCATA	1569
	TATGAATGGCTGACACTTCTTCCATGACTTTGGCAATCTGGGC TGCAGTGGTGGAGATCT**G**CAAACCTCGCTTTGAAGAAGTTCC TGGATTTTCTGTTGCTGGATGGTAGTTGCCTAGACC	1570
	GAGGTTTG**C**AGATCTCC	1571
	GGAGATCT**G**CAAACCTC	1572
Adenomatous polyposis coli Ser932Term TCA-TAA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATT**C**AAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1573
	GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTTT**G**AATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1574
	TACACATT**C**AAACACTT	1575
	AAGTGTTT**G**AATGTGTA	1576
Adenomatous polyposis coli Ser932Term TCA-TGA	TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATT**C**AAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC	1577

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTTT**G**AATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA	1578
	TACACATT**C**AAACACTT	1579
	AAGTGTTT**G**AATGTGTA	1580
Adenomatous polyposis coli Tyr935Term TAC-TAG	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTA**C**AATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1581
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATT**G**TAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1582
	AACACTTA**C**AATTTCAC	1583
	GTGAAATT**G**TAAGTGTT	1584
Adenomatous polyposis coli Tyr935Term TAC-TAA	GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCA TACACATTCAAACACTTA**C**AATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA	1585
	TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATT**G**TAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC	1586
	AACACTTA**C**AATTTCAC	1587
	GTGAAATT**G**TAAGTGTT	1588
Adenomatous polyposis coli Tyr1000Term TAC-TAA	ACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTAAGTTTT GCAGTTATGGTCAATA**C**CCAGCCGACCTAGCCCATAAAATACA TAGTGCAAATCATATGGATGATAATGATGGAGAA	1589
	TTCTCCATCATTATCATCCATATGATTTGCACTATGTATTTTAT GGGCTAGGTCGGCTGG**G**TATTGACCATAACTGCAAAACTTAC TTTCATCATCTTCAGAATAGGATTCAATCGAGGGT	1590
	GGTCAATA**C**CCAGCCGA	1591
	TCGGCTGG**G**TATTGACC	1592
Adenomatous polyposis coli Glu1020Term GAA-TAA	TACCCAGCCGACCTAGCCCATAAAATACATAGTGCAAATCATA TGGATGATAATGATGGA**G**AACTAGATACACCAATAAATTATAG TCTTAAATATTCAGATGAGCAGTTGAACTCTGGAA	1593
	TTCCAGAGTTCAACTGCTCATCTGAATATTTAAGACTATAATTT ATTGGTGTATCTAGTT**C**TCCATCATTATCATCCATATGATTTGC ACTATGTATTTTATGGGCTAGGTCGGCTGGGTA	1594
	ATGATGGA**G**AACTAGAT	1595
	ATCTAGTT**C**TCCATCAT	1596
Adenomatous polyposis coli Ser1032Term TCA-TAA	ATGAAACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTA AGTTTTGCAGTTATGGT**C**AATACCCAGCCGACCTAGCCCATAA AATACATAGTGCAAATCATATGGATGATAATGATG	1597
	CATCATTATCATCCATATGATTTGCACTATGTATTTTATGGGCT AGGTCGGCTGGGTATT**G**ACCATAACTGCAAAACTTACTTTCAT CATCTTCAGAATAGGATTCAATCGAGGGTTTCAT	1598

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTTATGGT**C**AATACCCA	1599
	TGGGTATT**G**ACCATAAC	1600
Adenomatous polyposis coli Gln1041Term CAA-TAA	TGAAGATGATGAAAGTAAGTTTTGCAGTTATGGTCAATACCCA GCCGACCTAGCCCATAA**A**ATACATAGTGCAAATCATATGGATG ATAATGATGGAGAACTAGATACACCAATAAATTAT	1601
	ATAATTTATTGGTGTATCTAGTTCTCCATCATTATCATCCATAT GATTTGCACTATGTAT**T**TTATGGGCTAGGTCGGCTGGGTATTG ACCATAACTGCAAAACTTACTTTCATCATCTTCA	1602
	GCCCATAA**A**ATACATAG	1603
	CTATGTAT**T**TTATGGGC	1604
Adenomatous polyposis coli Gln1045Term CAG-TAG	ATAAATTATAGTCTTAAATATTCAGATGAGCAGTTGAACTCTGG AAGGCAAAGTCCTTCA**C**AGAATGAAAGATGGGCAAGACCCAA ACACATAATAGAAGATGAAATAAAACAAAGTGAGC	1605
	GCTCACTTTGTTTTATTTCATCTTCTATTATGTGTTTGGGTCTT GCCCATCTTTCATTCT**G**TGAAGGACTTTGCCTTCCAGAGTTCA ACTGCTCATCTGAATATTTAAGACTATAATTTAT	1606
	GTCCTTCA**C**AGAATGAA	1607
	TTCATTCT**G**TGAAGGAC	1608
Adenomatous polyposis coli Gln1067Term CAA-TAA	GAAAGATGGGCAAGACCCAAACACATAATAGAAGATGAAATAA AACAAAGTGAGCAAAGA**C**AATCAAGGAATCAAAGTACAACTTA TCCTGTTTATACTGAGAGCACTGATGATAAACACC	1609
	GGTGTTTATCATCAGTGCTCTCAGTATAAACAGGATAAGTTGT ACTTTGATTCCTTGATT**G**TCTTTGCTCACTTTGTTTTATTTCATC TTCTATTATGTGTTTGGGTCTTGCCCATCTTTC	1610
	AGCAAAGA**C**AATCAAGG	1611
	CCTTGATT**G**TCTTTGCT	1612
Adenomatous polyposis coli Tyr1075Term TAT-TAG	AATAGAAGATGAAATAAAACAAAGTGAGCAAAGACAATCAAGG AATCAAAGTACAACTTA**T**CCTGTTTATACTGAGAGCACTGATG ATAAACACCTCAAGTTCCAACCACATTTTGGACAG	1613
	CTGTCCAAAATGTGGTTGGAACTTGAGGTGTTTATCATCAGTG CTCTCAGTATAAACAGG**A**TAAGTTGTACTTTGATTCCTTGATTG TCTTTGCTCACTTTGTTTTATTTCATCTTCTATT	1614
	ACAACTTA**T**CCTGTTTA	1615
	TAAACAGG**A**TAAGTTGT	1616
Adenomatous polyposis coli Tyr1102Term TAC-TAG	TGATGATAAACACCTCAAGTTCCAACCACATTTTGGACAGCAG GAATGTGTTTCTCCATA**C**AGGTCACGGGGAGCCAATGGTTCA GAAACAAATCGAGTGGGTTCTAATCATGGAATTAAT	1617
	ATTAATTCCATGATTAGAACCCACTCGATTTGTTTCTGAACCAT TGGCTCCCCGTGACCT**G**TATGGAGAAACACATTCCTGCTGTC CAAAATGTGGTTGGAACTTGAGGTGTTTATCATCA	1618
	TCTCCATA**C**AGGTCACG	1619
	CGTGACCT**G**TATGGAGA	1620

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Ser1110Term TCA-TGA	AACCACATTTTGGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTT**C**AGAAACAAATCGAGTGGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTG	1621
	CACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAACCCACTCGATTTGTTTCT**G**AACCATTGGCTCCCCGTGACCTGTATGGAGAAACACATTCCTGCTGTCCAAAATGTGGTT	1622
	CAATGGTT**C**AGAAACAA	1623
	TTGTTTCT**G**AACCATTG	1624
Adenomatous polyposis coli Arg1114Term CGA-TGA	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCAGAAACAAAT**C**GAGTGGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTGTCAAGAAGATG	1625
	CATCTTCTTGACACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAACCCACTC**G**ATTTGTTTCTGAACCATTGGCTCCCCGTGACCTGTATGGAGAAACACATTCCTGCTGTCC	1626
	AAACAAAT**C**GAGTGGGT	1627
	ACCCACTC**G**ATTTGTTT	1628
Adenomatous polyposis coli Tyr1135Term TAT-TAG	GGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTGTCAAGAAGATGACTA**T**GAAGATGATAAGCCTACCAATTATAGTGAACGTTACTCTGAAGAAGAACAGCATGAAGAA	1629
	TTCTTCATGCTGTTCTTCTTCAGAGTAACGTTCACTATAATTGGTAGGCTTATCATCTTC**A**TAGTCATCTTCTTGACACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAACCC	1630
	GATGACTA**T**GAAGATGA	1631
	TCATCTTC**A**TAGTCATC	1632
Adenomatous polyposis coli Gln1152Term CAG-TAG	GAAGATGACTATGAAGATGATAAGCCTACCAATTATAGTGAACGTTACTCTGAAGAAGAA**C**AGCATGAAGAAGAAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAAACGTC	1633
	GACGTTTCTCTTCATTATATTTTATGCTATAATTTGTTGGTCTCTCTTCTTCTTCATGCT**G**TTCTTCTTCAGAGTAACGTTCACTATAATTGGTAGGCTTATCATCTTCATAGTCATCTTC	1634
	AAGAAGAA**C**AGCATGAA	1635
	TTCATGCT**G**TTCTTCTT	1636
Adenomatous polyposis coli Gln1175Term CAG-TAG	GAAGAAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAAACGTCATGTGGAT**C**AGCCTATTGATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAACAGTCAT	1637
	ATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAAACTATAATCAATAGGCT**G**ATCCACATGACGTTTCTCTTCATTATATTTTATGCTATAATTTGTTGGTCTCTCTTCTTC	1638
	ATGTGGAT**C**AGCCTATT	1639
	AATAGGCT**G**ATCCACAT	1640

Clinical Phenotype & *Mutation*	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Pro1176Leu CCT-CTT	AAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAAACGTCATGTGGATCAGC**C**TATTGATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAACAGTCATTTTC	1641
	GAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAAACTATAATCAATA**G**GCTGATCCACATGACGTTTCTCTTCATTATATTTTATGCTATAATTTGTTGGTCTCTCTT	1642
	GGATCAGC**C**TATTGATT	1643
	AATCAATA**G**GCTGATCC	1644
Adenomatous polyposis coli Ala1184Pro GCC-CCC	ATAAAATATAATGAAGAGAAACGTCATGTGGATCAGCCTATTGATTATAGTTTAAAATAT**G**CCACAGATATTCCTTCATCACAGAAACAGTCATTTTCATTCTCAAAGAGTTCATCTGGAC	1645
	GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGG**C**ATATTTTAAACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCATTATATTTTAT	1646
	TAAAATAT**G**CCACAGAT	1647
	ATCTGTGG**C**ATATTTTA	1648
Adenomatous polyposis coli Ser1194Term TCA-TGA	ATCAGCCTATTGATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAACAGT**C**ATTTTCATTCTCAAAGAGTTCATCTGGACAAAGCAGTAAAACCGAACATATGTCTTCAAG	1649
	CTTGAAGACATATGTTCGGTTTTACTGCTTTGTCCAGATGAACTCTTTGAGAATGAAAAT**G**ACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAAACTATAATCAATAGGCTGAT	1650
	GAAACAGT**C**ATTTTCAT	1651
	ATGAAAAT**G**ACTGTTTC	1652
Adenomatous polyposis coli Ser1198Term TCA-TGA	ATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAACAGTCATTTTCATTCT**C**AAAGAGTTCATCTGGACAAAGCAGTAAAACCGAACATATGTCTTCAAGCAGTGAGAATAC	1653
	GTATTCTCACTGCTTGAAGACATATGTTCGGTTTTACTGCTTTGTCCAGATGAACTCTTT**G**AGAATGAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAAACTATAAT	1654
	TTCATTCT**C**AAAGAGTT	1655
	AACTCTTT**G**AGAATGAA	1656
Adenomatous polyposis coli Gln1228Term CAG-TAG	ACCGAACATATGTCTTCAAGCAGTGAGAATACGTCCACACCTTCATCTAATGCCAAGAGG**C**AGAATCAGCTCCATCCAGTTCTGCACAGAGTAGAAGTGGTCAGCCTCAAAGGCTGCCACT	1657
	AGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGTGCAGAACTGGATGGAGCTGATTCT**G**CCTCTTGGCATTAGATGAAGGTGTGGACGTATTCTCACTGCTTGAAGACATATGTTCGGT	1658
	CCAAGAGG**C**AGAATCAG	1659
	CTGATTCT**G**CCTCTTGG	1660

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1230Term CAG-TAG	CATATGTCTTCAAGCAGTGAGAATACGTCCACACCTTCATCTAATGCCAAGAGGCAGAAT**C**AGCTCCATCCAGTTCTGCACAGAGTAGAAGTGGTCAGCCTCAAAGGCTGCCACTTGCAAG	1661
	CTTGCAAGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGTGCAGAACTGGATGGAGCT**G**ATTCTGCCTCTTGGCATTAGATGAAGGTGTGGACGTATTCTCACTGCTTGAAGACATATG	1662
	GGCAGAAT**C**AGCTCCAT	1663
	ATGGAGCT**G**ATTCTGCC	1664
Adenomatous polyposis coli Cys1249Term TGC-TGA	TCAGCTCCATCCAAGTTCTGCACAGAGTAGAAGTGGTCAGCCTCAAAAGGCTGCCACTTG**C**AAAGTTTCTTCTATTAACCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATA	1665
	TATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTTCTTGGTTAATAGAAGAAACTTT**G**CAAGTGGCAGCCTTTTGAGGCTGACCACTTCTACTCTGTGCAGAACTTGGATGGAGCTGA	1666
	GCCACTTG**C**AAAGTTTC	1667
	GAAACTTT**G**CAAGTGGC	1668
Adenomatous polyposis coli Cys1270Term TGT-TGA	AGTTTCTTCTATTAACCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATG**T**TTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGAAGATGAAATAGGATGTAAT	1669
	ATTACATCCTATTTCATCTTCAGCTGATGACAAAGATGATAATGAACTACATCTTGAAAA**A**CATATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTTCTTGGTTAATAGAAGAAACT	1670
	CCAATATG**T**TTTTCAAG	1671
	CTTGAAAA**A**CATATTGG	1672
Adenomatous polyposis coli Ser1276Term TCA-TGA	AAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATGTTTTTCAAGATGTAGTT**C**ATTATCATCTTTGTCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACAGGAAGC	1673
	GCTTCCTGTGTCGTCTGATTACATCCTATTTCATCTTCAGCTGATGACAAAGATGATAAT**G**AACTACATCTTGAAAAACATATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTTCTT	1674
	ATGTAGTT**C**ATTATCAT	1675
	ATGATAAT**G**AACTACAT	1676
Adenomatous polyposis coli Glu1286Term GAA-TAA	GATACTCCAATATGTTTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGAAGAT**G**AAATAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATACCCTGCAAATAGCAG	1677
	CTGCTATTTGCAGGGTATTAGCAGAATCTGCTTCCTGTGTCGTCTGATTACATCCTATTT**C**ATCTTCAGCTGATGACAAAGATGATAATGAACTACATCTTGAAAAACATATTGGAGTATC	1678
	CTGAAGAT**G**AAATAGGA	1679
	TCCTATTT**C**ATCTTCAG	1680

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1294Term CAG-TAG	TGTAGTTCATTATCATCTTTGTCATCAGCTGAAGATGAAATAGG ATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATACCCTG CAAATAGCAGAAATAAAAGAAAAGATTGGAACTA	1681
	TAGTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTA GCAGAATCTGCTTCCTGTGTCGTCTGATTACATCCTATTTCAT CTTCAGCTGATGACAAAGATGATAATGAACTACA	1682
	AGACGACACAGGAAGCA	1683
	TGCTTCCTGTGTCGTCT	1684
Predisposition to, association with, colorectal cancer Ile1307Lys ATA-AAA	TAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATAC CCTGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTAGGTCA GCTGAAGATCCTGTGAGCGAAGTTCCAGCAGTGTC	1685
	GACACTGCTGGAACTTCGCTCACAGGATCTTCAGCTGACCTA GTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTAGC AGAATCTGCTTCCTGTGTCGTCTGATTACATCCTA	1686
	AGCAGAAATAAAAGAAA	1687
	TTTCTTTTATTTCTGCT	1688
Adenomatous polyposis coli Glu1309Term GAA-TAA	CCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATA TGTTTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGA AGATGAAATAGGATGTAATCAGACGACACAGGAA	1689
	TTCCTGTGTCGTCTGATTACATCCTATTTCATCTTCAGCTGATG ACAAAGATGATAATGAACTACATCTTGAAAAACATATTGGAGTA TCTTCTACACAATAAGTCTGTATTGTTTCTTGG	1690
	AGATGTAGTTCATTATC	1691
	GATAATGAACTACATCT	1692
Predisposition to Colorectal Cancer Glu1317Gln GAA-CAA	GATTCTGCTAATACCCTGCAAATAGCAGAAATAAAAGAAAAGA TTGGAACTAGGTCAGCTGAAGATCCTGTGAGCGAAGTTCCAG CAGTGTCACAGCACCCTAGAACCAAATCCAGCAGAC	1693
	GTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAA CTTCGCTCACAGGATCTTCAGCTGACCTAGTTCCAATCTTTTC TTTTATTTCTGCTATTTGCAGGGTATTAGCAGAATC	1694
	GGTCAGCTGAAGATCCT	1695
	AGGATCTTCAGCTGACC	1696
Adenomatous polyposis coli Gln1328Term CAG-TAG	AAAGAAAAGATTGGAACTAGGTCAGCTGAAGATCCTGTGAGC GAAGTTCCAGCAGTGTCACAGCACCCTAGAACCAAATCCAGC AGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCA	1697
	TGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTGG ATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACTTCGCTCA CAGGATCTTCAGCTGACCTAGTTCCAATCTTTTCTTT	1698
	CAGTGTCACAGCACCCT	1699
	AGGGTGCTGTGACACTG	1700

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Gln1338Term CAG-TAG	GATCCTGTGAGCGAAGTTCCAGCAGTGTCACAGCACCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAG	1701
	CTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACTTCGCTCACAGGATC	1702
	GCAGACTGCAGGGTTCT	1703
	AGAACCCTGCAGTCTGC	1704
Adenomatous polyposis coli Leu1342Term TTA-TAA	AAGTTCCAGCAGTGTCACAGCACCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTC	1705
	GAGGGAGATTTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACTT	1706
	TTCTAGTTTATCTTCAG	1707
	CTGAAGATAAACTAGAA	1708
Adenomatous polyposis coli Arg1348Trp AGG-TGG	CAGCACCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAG	1709
	CTGAGCACCACTTTCGGGAGGGAGATTTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTGGATTTGGTTCTAGGGTGCTG	1710
	AATCAGCCAGGCACAAA	1711
	TTTGTGCCTGGCTGATT	1712
Adenomatous polyposis coli Gly1357Term GGA-TGA	CTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAGACACCCCAAAGTCCACCTGAACACTAT	1713
	ATAGTGTTCAGGTGGACTTTGGGGTGTCTGAGCACCACTTTCGGGAGGGAGATTTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAG	1714
	TTTCTTCAGGAGCGAAA	1715
	TTTCGCTCCTGAAGAAA	1716
Adenomatous polyposis coli Gln1367Term CAG-TAG	CCAGGCACAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAGACACCCCAAAGTCCACCTGAACACTATGTTCAGGAGACCCCACTCATGTTTAGCAGAT	1717
	ATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTCAGGTGGACTTTGGGGTGTCTGAGCACCACTTTCGGGAGGGAGATTTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGG	1718
	GTGGTGCTCAGACACCC	1719
	GGGTGTCTGAGCACCAC	1720

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Adenomatous polyposis coli Lys1370Term AAA-TAA	AAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCAAAAGTGGTGCTCAGACACCC**A**AAAGTCCACCTGAACACTATGTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTG	1721
	CAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTCAGGTGGACTTT**T**GGGTGTCTGAGCACCACTTTTGGAGGGAGATTTCGCTCCTGAAGAAAATTCAACAGCTTT	1722
	AGACACCC**A**AAAGTCCA	1723
	TGGACTTT**T**GGGTGTCT	1724
Adenomatous polyposis coli Ser1392Term TCA-TAA	CACCTGAACACTATGTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCAGTT**C**ACTTGATAGTTTTGAGAGTCGTTCGATTGCCAGCTCCGTTCAGAGTGAACCATGCAGTGG	1725
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGACTCTCAAAACTATCAAGT**G**AACTGACAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTCAGGTG	1726
	TGTCAGTT**C**ACTTGATA	1727
	TATCAAGT**G**AACTGACA	1728
Adenomatous polyposis coli Ser1392Term TCA-TGA	CACCTGAACACTATGTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCAGTT**C**ACTTGATAGTTTTGAGAGTCGTTCGATTGCCAGCTCCGTTCAGAGTGAACCATGCAGTGG	1729
	CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGACTCTCAAAACTATCAAGT**G**AACTGACAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTCAGGTG	1730
	TGTCAGTT**C**ACTTGATA	1731
	TATCAAGT**G**AACTGACA	1732
Adenomatous polyposis *coli* Glu1397Term GAG-TAG	GTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCAGTTCACTTGATAGTTTT**G**AGAGTCGTTCGATTGCCAGCTCCGTTCAGAGTGAACCATGCAGTGGAATGGTAGGTGGCA	1733
	TGCCACCTACCATTCCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGACTCT**C**AAAACTATCAAGTGAACTGACAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAAC	1734
	ATAGTTTT**G**AGAGTCGT	1735
	ACGACTCT**C**AAAACTAT	1736
Adenomatous polyposis coli Lys1449Term AAG-TAG	CAAACCATGCCACCAAGCAGAAGTAAAACACCTCCACCACCTCCTCAAACAGCTCAAACC**A**AGCGAGAAGTACCTAAAAATAAAGCACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGC	1737
	GCTTAGGTCCACTCTCTCTCTTTTCAGCAGTAGGTGCTTTATTTTTAGGTACTTCTCGCT**T**GGTTTGAGCTGTTTGAGGAGGTGGTGGAGGTGTTTTACTTCTGCTTGGTGGCATGGTTTG	1738
	CTCAAACC**A**AGCGAGAA	1739
	TTCTCGCT**T**GGTTTGAG	1740
Adenomatous polyposis coli Arg1450Term CGA-TGA	ACCATGCCACCAAGCAGAAGTAAAACACCTCCACCACCTCCTCAAACAGCTCAAACCAAG**C**GAGAAGTACCTAAAAATAAAGCACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGCAAG	1741

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTGCTTAGGTCCACTCTCTCTCTTTTCAGCAGTAGGTGCTTTATTTTTAGGTACTTCTC**G**CTTGGTTTGAGCTGTTTGAGGAGGTGGTGGAGGTGTTTTACTTCTGCTTGGTGGCATGGT	1742
	AAACCAAG**C**GAGAAGTA	1743
	TACTTCTC**G**CTTGGTTT	1744
Adenomatous polyposis coli Ser1503Term TCA-TAA	CAGATGCTGATACTTTATTACATTTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTT**C**ATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAG	1745
	CTTAATTCCACATCTTTCTGTATAAATGGCTCATCGAGGCTCAGAGCACTCAGGCTGGAT**G**AACAAGAAAATCCATCTGGAGTACTTTCCGTGGCAAAATGTAATAAAGTATCAGCATCTG	1746
	TTCTTGTT**C**ATCCAGCC	1747
	GGCTGGAT**G**AACAAGAA	1748
Adenomatous polyposis coli Gln1529Term CAG-TAG	CTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAATAATGCCTCCAGTT**C**AGGAAAATGACAATGGGAATGAAACAGAATCAGAGCAGCCTAAAGAATCAAATGAAAACC	1749
	GGTTTTCATTTGATTCTTTAGGCTGCTCTGATTCTGTTTCATTCCCATTGTCATTTTCCT**G**AACTGGAGGCATTATTCTTAATTCCACATCTTTCTGTATAAATGGCTCATCGAGGCTCAG	1750
	CTCCAGTT**C**AGGAAAAT	1751
	ATTTTCCT**G**AACTGGAG	1752
Adenomatous polyposis coli Ser1539Term TCA-TAA	ATGTGGAATTAAGAATAATGCCTCCAGTTCAGGAAAATGACAATGGGAATGAAACAGAAT**C**AGAGCAGCCTAAAGAATCAAATGAAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTC	1753
	GAATCAATAGTTTTTTCTGCCTCTTTCTCTTGGTTTTCATTTGATTCTTTAGGCTGCTCT**G**ATTCTGTTTCATTCCCATTGTCATTTTCCTGAACTGGAGGCATTATTCTTAATTCCACAT	1754
	AACAGAAT**C**AGAGCAGC	1755
	GCTGCTCT**G**ATTCTGTT	1756
Adenomatous polyposis coli Ser1567Term TCA-TGA	AAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCTGAAAAGGACCTATTAGATGATT**C**AGATGATGATGATATTGAAATACTAGAAGAATGTATTATTTCTGCCATGCCAACAAAGTC	1757
	GACTTTGTTGGCATGGCAGAAATAATACATTCTTCTAGTATTTCAATATCATCATCATCT**G**AATCATCTAATAGGTCCTTTTCAGAATCAATAGTTTTTTCTGCCTCTTTCTCTTGGTTTT	1758
	AGATGATT**C**AGATGATG	1759
	CATCATCT**G**AATCATCT	1760
Adenomatous polyposis coli Asp1822Val GAC-GTC	AGAGAGTTTTCTCAGACAACAAAGATTCAAAGAAACAGAATTTGAAAAATAATTCCAAGG**A**CTTCAATGATAAGCTCCCAAATAATGAAGATAGAGTCAGAGGAAGTTTTGCTTTTGATTC	1761

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAATCAAAAGCAAAACTTCCTCTGACTCTATCTTCATTATTTGG GAGCTTATCATTGAAGTCCTTGGAATTATTTTTCAAATTCTGTT TCTTTGAATCTTTGTTGTCTGAGAAAACTCTCT	1762
	TTCCAAGGACTTCAATG	1763
	CATTGAAGTCCTTGGAA	1764
Adenomatous polyposis coli Leu2839Phe CTT-TTT	AAAACTGACAGCACAGAATCCAGTGGAACCCAAAGTCCTAAG CGCCATTCTGGGTCTTACCTTGTGACATCTGTTTAAAAGAGAG GAAGAATGAAACTAAGAAAATTCTATGTTAATTACA	1765
	TGTAATTAACATAGAATTTTCTTAGTTTCATTCTTCCTCTCTTTT AAACAGATGTCACAAGGTAAGACCCAGAATGGCGCTTAGGAC TTTGGGTTCCACTGGATTCTGTGCTGTCAGTTTT	1766
	GGTCTTACCTTGTGACA	1767
	TGTCACAAGGTAAGACC	1768

EXAMPLE 12
Parahemophilia - Factor V Deficiency

Deficiency in clotting Factor V is associated with a lifelong predisposition to thrombosis. The disease typically manifests itself with usually mild bleeding, although bleeding times and clotting times are consistently prolonged. Individuals that are heterozygous for a mutation in Factor V have lowered levels of factor V but probably never have abnormal bleeding. A large number of alleles with a range of presenting symptoms have been identified. The attached table discloses the correcting oligonucleotide base sequences for the Factor V oligonucleotides of the invention.

Table 19
Factor V Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Factor V deficiency Ala221Val GCC-GTC	TTGACTGAATGCTTATTTTGGCCTGTGTCTCTCCCTCTTTCTCA GATATAACAGTTTGTGCCCATGACCACATCAGCTGGCATCTGC TGGGAATGAGCTCGGGGCCAGAATTATTCTCCAT	4340
	ATGGAGAATAATTCTGGCCCCGAGCTCATTCCCAGCAGATGC CAGCTGATGTGGTCATGGGCACAAACTGTTATATCTGAGAAAG AGGGAGAGACACAGGCCAAAATAAGCATTCAGTCAA	1769
	AGTTTGTGCCCATGACC	1770
	GGTCATGGGCACAAACT	1771
Thrombosis Arg306Gly [illegible]	TGTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA ACTGCCCAAAGAAAACCAGGAATCTTAAGAAAATAACTCGTGA [illegible]	1772

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGAGT TATTTTCTTAAGATTCC**T**GGTTTTCTTTGGGCAGTTTTTAATGT CAATGTAAGCCTGCATCCCAGCTGAGTTAGGACA	1773
	AGAAAACC**A**GGAATCTT	1774
	AAGATTCC**T**GGTTTTCT	1775
Thrombosis Arg306Thr AGG-ACG	GTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAAA CTGCCCAAAGAAAACCA**G**GAATCTTAAGAAAATAACTCGTGAG CAGAGGCGGCACATGAAGAGGTGGGAATACTTCAT	1776
	ATGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGA GTTATTTTCTTAAGATTC**C**TGGTTTTCTTTGGGCAGTTTTTAAT GTCAATGTAAGCCTGCATCCCAGCTGAGTTAGGAC	1777
	GAAAACCA**G**GAATCTTA	1778
	TAAGATTC**C**TGGTTTTC	1779
Increased Risk Thrombosis Arg485Lys AGA-AAA	CCACAGAAAATGATGCCCAGTGCTTAACAAGACCATACTACAG TGACGTGGACATCATGA**G**AGACATCGCCTCTGGGCTAATAGG ACTACTTCTAATCTGTAAGAGCAGATCCCTGGACAG	1780
	CTGTCCAGGGATCTGCTCTTACAGATTAGAAGTAGTCCTATTA GCCCAGAGGCGATGTCT**C**TCATGATGTCCACGTCACTGTAGT ATGGTCTTGTTAAGCACTGGGCATCATTTTCTGTGG	1781
	CATCATGA**G**AGACATCG	1782
	CGATGTCT**C**TCATGATG	1783
Increased Risk Thrombosis Arg506Gln CGA-CAA	ACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGAG CAGATCCCTGGACAGGC**G**AGGAATACAGGTATTTTGTCCTTG AAGTAACCTTTCAGAAATTCTGAGAATTTCTTCTGG	1784
	CCAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGAC AAAATACCTGTATTCCT**C**GCCTGTCCAGGGATCTGCTCTTACA GATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGT	1785
	GGACAGGC**G**AGGAATAC	1786
	GTATTCCT**C**GCCTGTCC	1787
Factor V Deficiency Arg506Term CGA-TGA	GACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGA GCAGATCCCTGGACAGG**C**GAGGAATACAGGTATTTTGTCCTT GAAGTAACCTTTCAGAAATTCTGAGAATTTCTTCTG	1788
	CAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGACA AAATACCTGTATTCCTC**G**CCTGTCCAGGGATCTGCTCTTACAG ATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGTC	1789
	TGGACAGG**C**GAGGAATA	1790
	TATTCCTC**G**CCTGTCCA	1791
Thrombosis Arg712Term CGA-TGA	AGTGATGCTGACTATGATTACCAGAACAGACTGGCTGCAGCA TTAGGAATCAGGTCATTC**C**GAAACTCATCATTGAATCAGGAAG AAGAAGAGTTCAATCTTACTGCCCTAGCTCTGGAGA	1792
	TCTCCAGAGCTAGGGCAGTAAGATTGAACTCTTCTTCTTCCTG ATTCAATGATGAGTTTC**G**GAATGACCTGATTCCTAATGCTGCA GCCAGTCTGTTCTGGTAATCATAGTCAGCATCACT	1793
	GGTCATTC**C**GAAACTCA	1794

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAGTTTCGGAATGACC	1795
Thrombosis His1299Arg CAT-CGT	TCAGTCAGACAAACCTTTCCCCAGCCCTCGGTCAGATGCCCA TTTCTCCAGACCTCAGCCATACAACCCTTTCTCTAGACTTCAG CCAGACAAACCTCTCTCCAGAACTCAGTCAAACAAA	1796
	TTTGTTTGACTGAGTTCTGGAGAGAGGTTTGTCTGGCTGAAGT CTAGAGAAAGGGTTGTATGGCTGAGGTCTGGAGAAATGGGCA TCTGACCGAGGGCTGGGGAAAGGTTTGTCTGACTGA	1797
	CCTCAGCCATACAACCC	1798
	GGGTTGTATGGCTGAGG	1799

EXAMPLE 13
Hemophilia - Factor VIII Deficiency

The attached table discloses the correcting oligonucleotide base sequences for the Factor VIII oligonucleotides of the invention.

Table 20
Factor VIII Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia A Tyr5Cys TAC-TGC	AGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTT TAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTC ATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCC	1800
	GGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGT TCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAG AATCGCAAAAGGCACAGAAAGAAGCAGGTGGAGAGCT	1801
	CAGAAGATACTACCTGG	1802
	CCAGGTAGTATCTTCTG	1803
Haemophilia A Leu7Arg CTG-CGG	CCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGC CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGA CTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGA	1804
	TCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCAT GACAGTTCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTA AAGCAGAATCGCAAAAGGCACAGAAAGAAGCAGGTGG	1805
	ATACTACCTGGGTGCAG	1806
	CTGCACCCAGGTAGTAT	1807
Haemophilia A Ser(-1)Arg AGTg-AGG	AGTCATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTT TTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGT GCAGTGGAACTGTCATGGGACTATATGCAAAGTGAT	1808

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAG GTAGTATCTTCTGGTGGC**A**CTAAAGCAGAATCGCAAAAGGCA CAGAAAGAAGCAGGTGGAGAGCTCTATTTGCATGACT	1809
	TGCTTTAG**T**GCCACCAG	1810
	CTGGTGGC**A**CTAAAGCA	1811
Haemophilia A Arg(-5)Term gCGA-TGA	CATTTGTAGCAATAAGTCATGCAAATAGAGCTCTCCACCTGCT TCTTTCTGTGCCTTTTG**C**GATTCTGCTTTAGTGCCACCAGAAG ATACTACCTGGGTGCAGTGGAACTGTCATGGGACT	1812
	AGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGG TGGCACTAAAGCAGAATC**G**CAAAAGGCACAGAAAGAAGCAGG TGGAGAGCTCTATTTGCATGACTTATTGCTACAAATG	1813
	GCCTTTTG**C**GATTCTGC	1814
	GCAGAATC**G**CAAAAGGC	1815
Haemophilia A Glu11Val GAA-GTA	TTCTGTGCCTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATA CTACCTGGGTGCAGTGG**A**ACTGTCATGGGACTATATGCAAAG TGATCTCGGTGAGCTGCCTGTGGACGCAAGGTAAAG	1816
	CTTTACCTTGCGTCCACAGGCAGCTCACCGAGATCACTTTGC ATATAGTCCCATGACAGT**T**CCACTGCACCCAGGTAGTATCTTC TGGTGGCACTAAAGCAGAATCGCAAAAGGCACAGAA	1817
	TGCAGTGG**A**ACTGTCAT	1818
	ATGACAGT**T**CCACTGCA	1819
Haemophilia A Trp14Gly aTGG-GGG	CTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACCTGG GTGCAGTGGAACTGTCA**T**GGGACTATATGCAAAGTGATCTCG GTGAGCTGCCTGTGGACGCAAGGTAAAGGCATGTCC	1820
	GGACATGCCTTTACCTTGCGTCCACAGGCAGCTCACCGAGAT CACTTTGCATATAGTCCC**A**TGACAGTTCCACTGCACCCAGGT AGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAAG	1821
	AACTGTCA**T**GGGACTAT	1822
	ATAGTCCC**A**TGACAGTT	1823
Haemophilia A Tyr46Term TACa-TAA	TTCACGCAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTC AACACCTCAGTCGTGTA**C**AAAAAGACTCTGTTTGTAGAATTCA CGGATCACCTTTTCAACATCGCTAAGCCAAGGCCA	1824
	TGGCCTTGGCTTAGCGATGTTGAAAAGGTGATCCGTGAATTC TACAAACAGAGTCTTTTT**G**TACACGACTGAGGTGTTGAATGGA AAAGATTTTGGCACTCTAGGAGGAAATCTGCGTGAA	1825
	GTCGTGTA**C**AAAAAGAC	1826
	GTCTTTTT**G**TACACGAC	1827
Haemophilia A Asp56Glu GATc-GAA	ATCTTTTCCATTCAACACCTCAGTCGTGTACAAAAAGACTCTG TTTGTAGAATTCACGGA**T**CACCTTTTCAACATCGCTAAGCCAA GGCCACCCTGGATGGGTAATGAAAACAATGTTGAA	1828

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCAACATTGTTTTCATTACCCATCCAGGGTGGCCTTGGCTTA GCGATGTTGAAAAGGTGATCCGTGAATTCTACAAACAGAGTC TTTTTGTACACGACTGAGGTGTTGAATGGAAAAGAT	1829
	TTCACGGATCACCTTTT	1830
	AAAAGGTGATCCGTGAA	1831
Haemophilia A Gly73Val GGT-GTT	TTCTGGAGTACTATCCCCAAGTAACCTTTGGCGGACATCTCAT TCTTACAGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA TGATACAGTGGTCATTACACTTAAGAACATGGCTTC	1832
	GAAGCCATGTTCTTAAGTGTAATGACCACTGTATCATAAACCT CAGCCTGGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT GTCCGCCAAAGGTTACTTGGGGATAGTACTCCAGAA	1833
	TCTGCTAGGTCCTACCA	1834
	TGGTAGGACCTAGCAGA	1835
Haemophilia A Glu79Lys tGAG-AAG	CAAGTAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAG GTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTAC ACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTC	1836
	GAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAATGA CCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCTAGCA GACCTGTAAGAATGAGATGTCCGCCAAAGGTTACTTG	1837
	TCCAGGCTGAGGTTTAT	1838
	ATAAACCTCAGCCTGGA	1839
Haemophilia A Val80Asp GTT-GAT	TAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCC TACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACTT AAGAACATGGCTTCCCATCCTGTCAGTCTTCATGC	1840
	GCATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTA ATGACCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCT AGCAGACCTGTAAGAATGAGATGTCCGCCAAAGGTTA	1841
	GGCTGAGGTTTATGATA	1842
	TATCATAAACCTCAGCC	1843
Haemophilia A Asp82Val GAT-GTT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAAC ATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1844
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1845
	GGTTTATGATACAGTGG	1846
	CCACTGTATCATAAACC	1847
Haemophilia A Asp82Gly GAT-GGT	TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAAC ATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG	1848

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA	1849
	GGTTTATGATACAGTGG	1850
	CCACTGTATCATAAACC	1851
Haemophilia A Val85Asp GTC-GAC	ATCTCATTCTTACAGGTCTGCTAGGTCCTACCATCCAGGCTGA GGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCC CATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTA	1852
	TAGGATACACCAACAGCATGAAGACTGACAGGATGGGAAGCC ATGTTCTTAAGTGTAATGACCACTGTATCATAAACCTCAGCCT GGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT	1853
	TACAGTGGTCATTACAC	1854
	GTGTAATGACCACTGTA	1855
Haemophilia A Lys89Thr AAG-ACG	CAGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATA CAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCA GTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTC	1856
	GAAGCTTTCCAGTAGGATACACCAACAGCATGAAGACTGACA GGATGGGAAGCCATGTTCTTAAGTGTAATGACCACTGTATCAT AAACCTCAGCCTGGATGGTAGGACCTAGCAGACCTG	1857
	TACACTTAAGAACATGG	1858
	CCATGTTCTTAAGTGTA	1859
Haemophilia A Met91Val cATG-GTG	CTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTG GTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTC ATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGG	1860
	CCTCAGAAGCTTTCCAGTAGGATACACCAACAGCATGAAGAC TGACAGGATGGGAAGCCATGTTCTTAAGTGTAATGACCACTG TATCATAAACCTCAGCCTGGATGGTAGGACCTAGCAG	1861
	TTAAGAACATGGCTTCC	1862
	GGAAGCCATGTTCTTAA	1863
Haemophilia A His94Arg CAT-CGT	CTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACT TAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGT GTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAAA	1864
	TTTTACTCACCCTCAGAAGCTTTCCAGTAGGATACACCAACAG CATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA TGACCACTGTATCATAAACCTCAGCCTGGATGGTAG	1865
	GGCTTCCCATCCTGTCA	1866
	TGACAGGATGGGAAGCC	1867
Haemophilia A His94Tyr cCAT-TAT	CCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACAC TTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG TGTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAA	1868

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTACTCACCCTCAGAAGCTTTCCAGTAGGATACACCAACAGC ATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAAT GACCACTGTATCATAAACCTCAGCCTGGATGGTAGG	1869
	TGGCTTCCCATCCTGTC	1870
	GACAGGATGGGAAGCCA	1871
Haemophilia A Leu98Arg CTT-CGT	CTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGC TTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGG AAAGCTTCTGAGGGTGAGTAAAATACCCTCCTATT	1872
	AATAGGAGGGTATTTTACTCACCCTCAGAAGCTTTCCAGTAGG ATACACCAACAGCATGAAGACTGACAGGATGGGAAGCCATGT TCTTAAGTGTAATGACCACTGTATCATAAACCTCAG	1873
	TGTCAGTCTTCATGCTG	1874
	CAGCATGAAGACTGACA	1875
Haemophilia A Gly102Ser tGGT-AGT	GATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTG TCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGA GGGTGAGTAAAATACCCTCCTATTGTCCTGTCATT	1876
	AATGACAGGACAATAGGAGGGTATTTTACTCACCCTCAGAAG CTTTCCAGTAGGATACACCAACAGCATGAAGACTGACAGGAT GGGAAGCCATGTTCTTAAGTGTAATGACCACTGTATC	1877
	ATGCTGTTGGTGTATCC	1878
	GGATACACCAACAGCAT	1879
Haemophilia A Glu113Asp GAAt-GAC	CTTTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTC CTGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGG AGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGC	1880
	GCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGA CTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAATA AAATTGTCCTTTCTATATCCACTGTACACTCAAAG	1881
	GGAGCTGAATATGATGA	1882
	TCATCATATTCAGCTCC	1883
Haemophilia A Tyr114Cys TAT-TGT	TTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTCCT GCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAG AAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCCA	1884
	TGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT GACTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAA TAAAATTGTCCTTTCTATATCCACTGTACACTCAA	1885
	AGCTGAATATGATGATC	1886
	GATCATCATATTCAGCT	1887
Haemophilia A Asp116Gly GAT-GGT	GTACAGTGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATA GGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAA GATGATAAAGTCTTCCCTGGTGGAAGCCATACATA	1888

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCT CCCTTTGACTGGTCTGA**T**CATCATATTCAGCTCCTATAGCAGG AAGAAATAAAATTGTCCTTTCTATATCCACTGTAC	1889
	ATATGATG**A**TCAGACCA	1890
	TGGTCTGA**T**CATCATAT	1891
Haemophilia A Gln117Term tCAG-TAG	ACAGTGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATAG GAGCTGAATATGATGAT**C**AGACCAGTCAAAGGGAGAAAGAAG ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATG	1892
	CATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTT CTCCCTTTGACTGGTCT**G**ATCATCATATTCAGCTCCTATAGCA GGAAGAAATAAAATTGTCCTTTCTATATCCACTGT	1893
	ATGATGAT**C**AGACCAGT	1894
	ACTGGTCT**G**ATCATCAT	1895
Haemophilia A Thr118Ile ACC-ATC	TGGATATAGAAAGGACAATTTTATTTCTTCCTGCTATAGGAGC TGAATATGATGATCAGA**C**CAGTCAAAGGGAGAAAGAAGATGA TAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTG	1896
	CAGACATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTT CTTTCTCCCTTTGACTG**G**TCTGATCATCATATTCAGCTCCTAT AGCAGGAAGAAATAAAATTGTCCTTTCTATATCCA	1897
	TGATCAGA**C**CAGTCAAA	1898
	TTTGACTG**G**TCTGATCA	1899
Haemophilia A Glu122Term gGAG-TAG	AGGACAATTTTATTTCTTCCTGCTATAGGAGCTGAATATGATG ATCAGACCAGTCAAAGG**G**AGAAAGAAGATGATAAAGTCTTCC CTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGA	1900
	TCAGGACCTGCCAGACATATGTATGGCTTCCACCAGGGAAGA CTTTATCATCTTCTTTCT**C**CCTTTGACTGGTCTGATCATCATAT TCAGCTCCTATAGCAGGAAGAAATAAAATTGTCCT	1901
	GTCAAAGG**G**AGAAAGAA	1902
	TTCTTTCT**C**CCTTTGAC	1903
Haemophilia A Asp126His tGAT-CAT	TTTCTTCCTGCTATAGGAGCTGAATATGATGATCAGACCAGTC AAAGGGAGAAAGAAGAT**G**ATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTC	1904
	GACCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTTCC ACCAGGGAAGACTTTAT**C**ATCTTCTTTCTCCCTTTGACTGGTC TGATCATCATATTCAGCTCCTATAGCAGGAAGAAA	1905
	AAGAAGAT**G**ATAAAGTC	1906
	GACTTTAT**C**ATCTTCTT	1907
Haemophilia A Gln139Term gCAG-TAG	AGTCAAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGA AGCCATACATATGTCTGG**C**AGGTCCTGAAAGAGAATGGTCCA ATGGCCTCTGACCCACTGTGCCTTACCTACTCATATC	1908

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTTCCAC CAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACT	1909
	ATGTCTGGCAGGTCCTG	1910
	CAGGACCTGCCAGACAT	1911
Haemophilia A Val140Ala GTC-GCC	AAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGG CCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC	1912
	GAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATT GGACCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTT CCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT	1913
	CTGGCAGGTCCTGAAAG	1914
	CTTTCAGGACCTGCCAG	1915
Haemophilia A Asn144Lys AATg-AAA	AGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTG GCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACT GTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG	1916
	CAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGG GTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAGAC ATATGTATGGCTTCCACCAGGGAAGACTTTATCATCT	1917
	AAAGAGAATGGTCCAAT	1918
	ATTGGACCATTCTCTTT	1919
Haemophilia AG Gly145Asp GGT-GAT	ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCA GGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTG CCTTACCTACTCATATCTTTCTCATGTGGACCTGGT	1920
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1921
	AGAGAATGGTCCAATGG	1922
	CCATTGGACCATTCTCT	1923
Haemophilia A Gly145Val GGT-GTT	ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCA GGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTG CCTTACCTACTCATATCTTTCTCATGTGGACCTGGT	1924
	ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGACCATTCTCTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT	1925
	AGAGAATGGTCCAATGG	1926
	CCATTGGACCATTCTCT	1927
Haemophilia A Pro146Ser tCCA-TCA	GATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAG GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTTCTCATGTGGACCTGGTAA	1928

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACA GTGGGTCAGAGGCCATTG**G**ACCATTCTCTTTCAGGACCTGCC AGACATATGTATGGCTTCCACCAGGGAAGACTTTATC	1929
	AGAATGGT**C**CAATGGCC	1930
	GGCCATTG**G**ACCATTCT	1931
Haemophilia A Cys153Trp TGCc-TGG	CCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAAT GGCCTCTGACCCACTGTG**C**CTTACCTACTCATATCTTTCTCAT GTGGACCTGGTAAAAGACTTGAATTCAGGCCTCATT	1932
	AATGAGGCCTGAATTCAAGTCTTTTACCAGGTCCACATGAGAA AGATATGAGTAGGTAAG**G**CACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTCAGGACCTGCCAGACATATGTATGG	1933
	CCACTGTG**C**CTTACCTA	1934
	TAGGTAAG**G**CACAGTGG	1935
Haemophilia A Tyr156Term TACt-TAA	TGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGA CCCACTGTGCCTTACCTA**C**TCATATCTTTCTCATGTGGACCTG GTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTA	1936
	TAGGGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGTC CACATGAGAAAGATATGA**G**TAGGTAAGGCACAGTGGGTCAGA GGCCATTGGACCATTCTCTTTCAGGACCTGCCAGACA	1937
	CTTACCTA**C**TCATATCT	1938
	AGATATGA**G**TAGGTAAG	1939
Haemophilia A Ser157Pro cTCA-CCA	GTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGAC CCACTGTGCCTTACCTAC**T**CATATCTTTCTCATGTGGACCTGG TAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTAC	1940
	GTAGGGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGT CCACATGAGAAAGATATG**A**GTAGGTAAGGCACAGTGGGTCAG AGGCCATTGGACCATTCTCTTTCAGGACCTGCCAGAC	1941
	TTACCTAC**T**CATATCTT	1942
	AAGATATG**A**GTAGGTAA	1943
Haemophilia A Ser160Pro tTCT-CCT	GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTT**T**CTCATGTGGACCTGGTAAAAGACT TGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTA	1944
	TACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAAGTCTTT TACCAGGTCCACATGAG**A**AAGATATGAGTAGGTAAGGCACAG TGGGTCAGAGGCCATTGGACCATTCTCTTTCAGGAC	1945
	CATATCTT**T**CTCATGTG	1946
	CACATGAG**A**AAGATATG	1947
Haemophilia A Val162Met tGTG-ATG	AAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACC TACTCATATCTTTCTCAT**G**TGGACCTGGTAAAAGACTTGAATT CAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAG	1948

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAA GTCTTTTACCAGGTCCA**C**ATGAGAAAGATATGAGTAGGTAAG GCACAGTGGGTCAGAGGCCATTGGACCATTCTCTTT	1949
	TTTCTCAT**G**TGGACCTG	1950
	CAGGTCCA**C**ATGAGAAA	1951
Haemophilia A Lys166Thr AAA-ACA	CAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC TCATGTGGACCTGGTAA**A**AGACTTGAATTCAGGCCTCATTGG AGCCCTACTAGTATGTAGAGAAGGTAAGTGTATGAA	1952
	TTCATACACTTACCTTCTCTACATACTAGTAGGGCTCCAATGA GGCCTGAATTCAAGTCT**T**TTACCAGGTCCACATGAGAAAGATA TGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTG	1953
	CCTGGTAA**A**AGACTTGA	1954
	TCAAGTCT**T**TTACCAGG	1955
Haemophilia A Ser170Leu TCA-TTA	ACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCT GGTAAAAGACTTGAATT**C**AGGCCTCATTGGAGCCCTACTAGT ATGTAGAGAAGGTAAGTGTATGAAAGCGTAGGATTG	1956
	CAATCCTACGCTTTCATACACTTACCTTCTCTACATACTAGTAG GGCTCCAATGAGGCCT**G**AATTCAAGTCTTTTACCAGGTCCAC ATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGT	1957
	CTTGAATT**C**AGGCCTCA	1958
	TGAGGCCT**G**AATTCAAG	1959
Haemophilia A Phe195Val aTTT-GTT	AATGTTCTCACTTCTTTTTCAGGGAGTCTGGCCAAGGAAAAGA CACAGACCTTGCACAAA**T**TTATACTACTTTTTGCTGTATTTGAT GAAGGTTAGTGAGTCTTAATCTGAATTTTGGATT	1960
	AATCCAAAATTCAGATTAAGACTCACTAACCTTCATCAAATACA GCAAAAAGTAGTATAA**A**TTTGTGCAAGGTCTGTGTCTTTTCCT TGGCCAGACTCCCTGAAAAAGAAGTGAGAACATT	1961
	TGCACAAA**T**TTATACTA	1962
	TAGTATAA**A**TTTGTGCA	1963
Haemophilia A Leu198His CTT-CAT	CTTCTTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCT TGCACAAATTTATACTAC**T**TTTTGCTGTATTTGATGAAGGTTAG TGAGTCTTAATCTGAATTTTGGATTCCTGAAAGAA	1964
	TTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACTAACCTTC ATCAAATACAGCAAAA**A**GTAGTATAAATTTGTGCAAGGTCTGT GTCTTTTCCTTGGCCAGACTCCCTGAAAAAGAAG	1965
	TATACTAC**T**TTTTGCTG	1966
	CAGCAAAA**A**GTAGTATA	1967
Haemophilia A Ala200Asp GCT-GAT	TTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCACA AATTTATACTACTTTTTG**C**TGTATTTGATGAAGGTTAGTGAGTC TTAATCTGAATTTTGGATTCCTGAAAGAAATCCTC	1968

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGGATTTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACT AACCTTCATCAAATACA**G**CAAAAAGTAGTATAAATTTGTGCAA GGTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAA	1969
	ACTTTTTG**C**TGTATTTG	1970
	CAAATACA**G**CAAAAAGT	1971
Haemophilia A Ala200Thr tGCT-ACT	TTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCAC AAATTTATACTACTTTTT**G**CTGTATTTGATGAAGGTTAGTGAGT CTTAATCTGAATTTTGGATTCCTGAAAGAAATCCT	1972
	AGGATTTCTTTCAGGAATCCAAAATTCAGATTAAGACTCACTA ACCTTCATCAAATACAG**C**AAAAAGTAGTATAAATTTGTGCAAG GTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAAA	1973
	TACTTTTT**G**CTGTATTT	1974
	AAATACAG**C**AAAAAGTA	1975
Haemophilia A Val234Phe aGTC-TTC	AACTCCTTGATGCAGGATAGGGATGCTGCATCTGCTCGGGCC TGGCCTAAAATGCACACA**G**TCAATGGTTATGTAAACAGGTCTC TGCCAGGTATGTACACACCTGCTCAACAATCCTCAG	1976
	CTGAGGATTGTTGAGCAGGTGTGTACATACCTGGCAGAGACC TGTTTACATAACCATTGA**C**TGTGTGCATTTTAGGCCAGGCCCG AGCAGATGCAGCATCCCTATCCTGCATCAAGGAGTT	1977
	TGCACACA**G**TCAATGGT	1978
	ACCATTGA**C**TGTGTGCA	1979
Haemophilia A Gly247Glu GGA-GAA	ATTTCAGATTCTCTACTTCATAGCCATAGGTGTCTTATTCCTAC TTTACAGGTCTGATTG**G**ATGCCACAGGAAATCAGTCTATTGGC ATGTGATTGGAATGGGCACCACTCCTGAAGTGCA	1980
	TGCACTTCAGGAGTGGTGCCCATTCCAATCACATGCCAATAG ACTGATTTCCTGTGGCAT**C**CAATCAGACCTGTAAAGTAGGAAT AAGACACCTATGGCTATGAAGTAGAGAATCTGAAAT	1981
	TCTGATTG**G**ATGCCACA	1982
	TGTGGCAT**C**CAATCAGA	1983
Haemophilia A Trp255Cys TGGc-TGT	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTG**G**CATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1984
	TGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT GCCCATTCCAATCACATG**C**CAATAGACTGATTTCCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1985
	GTCTATTG**G**CATGTGAT	1986
	ATCACATG**C**CAATAGAC	1987
Haemophilia A Trp255Term TGGc-TGA	ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTG**G**CATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA	1988

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT GCCCATTCCAATCACATGCCAATAGACTGATTTCCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT	1989
	GTCTATTGGCATGTGAT	1990
	ATCACATGCCAATAGAC	1991
Haemophilia A His256Leu CAT-CTT	AGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCACAG GAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCC TGAAGTGCACTCAATATTCCTCGAAGGTCACACATT	1992
	AATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTG GTGCCCATTCCAATCACATGCCAATAGACTGATTTCCTGTGG CATCCAATCAGACCTGTAAAGTAGGAATAAGACACCT	1993
	CTATTGGCATGTGATTG	1994
	CAATCACATGCCAATAG	1995
Haemophilia A Gly259Arg tGGA-AGA	TATTCCTACTTTACAGGTCTGATTGGATGCCACAGGAAATCAG TCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAGTGC ACTCAATATTCCTCGAAGGTCACACATTTCTTGTGA	1996
	TCACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACTTC AGGAGTGGTGCCCATTCCAATCACATGCCAATAGACTGATTT CCTGTGGCATCCAATCAGACCTGTAAAGTAGGAATA	1997
	ATGTGATTGGAATGGGC	1998
	GCCCATTCCAATCACAT	1999
Haemophilia A Val266Gly GTG-GGG	TTGGATGCCACAGGAAATCAGTCTATTGGCATGTGATTGGAAT GGGCACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCA CACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTT	2000
	AAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACTTCAGGAGTGGTGCCCATTCCA ATCACATGCCAATAGACTGATTTCCTGTGGCATCCAA	2001
	TCCTGAAGTGCACTCAA	2002
	TTGAGTGCACTTCAGGA	2003
Haemophilia A Glu272Gly GAA-GGA	CAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAG TGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAA CCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAAC	2004
	GTTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTC ACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAG GAGTGGTGCCCATTCCAATCACATGCCAATAGACTG	2005
	ATTCCTCGAAGGTCACA	2006
	TGTGACCTTCGAGGAAT	2007
Haemophilia A Glu272Lys cGAA-AAA	TCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGA ACCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAA	2008

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCA CAAGAAATGTGTGACCTT**C**GAGGAATATTGAGTGCACTTCAG GAGTGGTGCCCATTCCAATCACATGCCAATAGACTGA	2009
	TATTCCTC**G**AAGGTCAC	2010
	GTGACCTT**C**GAGGAATA	2011
Haemophilia A Thr275Ile ACA-ATA	GGCATGTGATTGGAATGGGCACCACTCCTGAAGTGCACTCAA TATTCCTCGAAGGTCACA**C**ATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAAATCTCGCCAATAACTTTCCTTAC	2012
	GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAAT**G**TGTGACCTTCGAGGAATATTGAGT GCACTTCAGGAGTGGTGCCCATTCCAATCACATGCC	2013
	AGGTCACA**C**ATTTCTTG	2014
	CAAGAAAT**G**TGTGACCT	2015
Haemophilia A Val278Ala GTG-GCG	TTGGAATGGGCACCACTCCTGAAGTGCACTCAATATTCCTCG AAGGTCACACATTTCTTG**T**GAGGAACCATCGCCAGGCGTCCT TGGAAATCTCGCCAATAACTTTCCTTACTGCTCAAAC	2016
	GTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCAAGGAC GCCTGGCGATGGTTCCTC**A**CAAGAAATGTGTGACCTTCGAGG AATATTGAGTGCACTTCAGGAGTGGTGCCCATTCCAA	2017
	ATTTCTTG**T**GAGGAACC	2018
	GGTTCCTC**A**CAAGAAAT	2019
Haemophilia A Asn280Ile AAC-ATC	TGGGCACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTC ACACATTTCTTGTGAGGA**A**CCATCGCCAGGCGTCCTTGGAAA TCTCGCCAATAACTTTCCTTACTGCTCAAACACTCTT	2020
	AAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCA AGGACGCCTGGCGATGG**T**TCCTCACAAGAAATGTGTGACCTT CGAGGAATATTGAGTGCACTTCAGGAGTGGTGCCCA	2021
	TGTGAGGA**A**CCATCGCC	2022
	GGCGATGG**T**TCCTCACA	2023
Haemophilia A Arg282Cys tCGC-TGC	ACCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACAT TTCTTGTGAGGAACCAT**C**GCCAGGCGTCCTTGGAAATCTCGC CAATAACTTTCCTTACTGCTCAAACACTCTTGATGG	2024
	CCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGA TTTCCAAGGACGCCTGGC**G**ATGGTTCCTCACAAGAAATGTGT GACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGGT	2025
	GGAACCAT**C**GCCAGGCG	2026
	CGCCTGGC**G**ATGGTTCC	2027
Haemophilia A Arg282His CGC-CAC	CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATC**G**CCAGGCGTCCTTGGAAATCTCGCC AATAACTTTCCTTACTGCTCAAACACTCTTGATGGA	2028

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGG	2029
	GAACCATCGCCAGGCGT	2030
	ACGCCTGGCGATGGTTC	2031
Haemophilia A Arg282Leu CGC-CTC	CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCC AATAACTTTCCTTACTGCTCAAACACTCTTGATGGA	2032
	TCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACTTCAGGAGTGG	2033
	GAACCATCGCCAGGCGT	2034
	ACGCCTGGCGATGGTTC	2035
Haemophilia A Ala284Glu GCG-GAG	CTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGT GAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAAC TTTCCTTACTGCTCAAACACTCTTGATGGACCTTGG	2036
	CCAAGGTCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATT GGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAG AAATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAG	2037
	TCGCCAGGCGTCCTTGG	2038
	CCAAGGACGCCTGGCGA	2039
Haemophilia A Ala284Pro gGCG-CCG	CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTG TGAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGCCAATAA CTTTCCTTACTGCTCAAACACTCTTGATGGACCTTG	2040
	CAAGGTCCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTG GCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAA ATGTGTGACCTTCGAGGAATATTGAGTGCACTTCAGG	2041
	ATCGCCAGGCGTCCTTG	2042
	CAAGGACGCCTGGCGAT	2043
Haemophilia A Ser289Leu TCG-TTG	TATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAAATCTCGCCAATAACTTTCCTTACTGCTCAA ACACTCTTGATGGACCTTGGACAGTTTCTACTGTT	2044
	AACAGTAGAAACTGTCCAAGGTCCATCAAGAGTGTTTGAGCA GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAATGTGTGACCTTCGAGGAATA	2045
	GGAAATCTCGCCAATAA	2046
	TTATTGGCGAGATTTCC	2047
Haemophilia A Phe293Ser TTC-TCC	GTCACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGG AAATCTCGCCAATAACTTTCCTTACTGCTCAAACACTCTTGAT GGACCTTGGACAGTTTCTACTGTTTTGTCATATCTC	2048

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGATATGACAAAACAGTAGAAACTGTCCAAGGTCCATCAAG AGTGTTTGAGCAGTAAGG**A**AAGTTATTGGCGAGATTTCCAAG GACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGAC	2049
	AATAACTT**T**CCTTACTG	2050
	CAGTAAGG**A**AAGTTATT	2051
Haemophilia A Thr295Ala tACT-GCT	ACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAAATC TCGCCAATAACTTTCCTT**A**CTGCTCAAACACTCTTGATGGACC TTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCC	2052
	GGGAAGAGATATGACAAAACAGTAGAAACTGTCCAAGGTCCA TCAAGAGTGTTTGAGCAG**T**AAGGAAAGTTATTGGCGAGATTTC CAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGT	2053
	CTTTCCTT**A**CTGCTCAA	2054
	TTGAGCAG**T**AAGGAAAG	2055
Haemophilia A Thr295Ile ACT-ATT	CATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAAATCT CGCCAATAACTTTCCTTA**C**TGCTCAAACACTCTTGATGGACCT TGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCA	2056
	TGGGAAGAGATATGACAAAACAGTAGAAACTGTCCAAGGTCC ATCAAGAGTGTTTGAGCA**G**TAAGGAAAGTTATTGGCGAGATTT CCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATG	2057
	TTTCCTTA**C**TGCTCAAA	2058
	TTTGAGCA**G**TAAGGAAA	2059
Haemophilia A Ala296Val GCT-GTT	TTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAAATCTCGC CAATAACTTTCCTTACTG**C**TCAAACACTCTTGATGGACCTTGG ACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA	2060
	TGGTGGGAAGAGATATGACAAAACAGTAGAAACTGTCCAAGG TCCATCAAGAGTGTTTGA**G**CAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAA	2061
	CCTTACTG**C**TCAAACAC	2062
	GTGTTTGA**G**CAGTAAGG	2063
Haemophilia A Leu308Pro CTG-CCG	TCTCGCCAATAACTTTCCTTACTGCTCAAACACTCTTGATGGA CCTTGGACAGTTTCTAC**T**GTTTTGTCATATCTCTTCCCACCAA CATGGTAATATCTTGGATCTTTAAAATGAATATTA	2064
	TAATATTCATTTTAAAGATCCAAGATATTACCATGTTGGTGGGA AGAGATATGACAAAAC**A**GTAGAAACTGTCCAAGGTCCATCAA GAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGA	2065
	GTTTCTAC**T**GTTTTGTC	2066
	GACAAAAC**A**GTAGAAAC	2067
Haemophilia A Glu321Lys gGAA-AAA	ACAGCCTAATATAGCAAGACACTCTGACATTGTTTGGTTTGTC TGACTCCAGATGGCATG**G**AAGCTTATGTCAAAGTAGACAGCT GTCCAGAGGAACCCCAACTACGAATGAAAAATAATG	2068

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CATTATTTTTCATTCGTAGTTGGGGTTCCTCTGGACAGCTGTC TACTTTGACATAAGCTT**C**CATGCCATCTGGAGTCAGACAAACC AAACAATGTCAGAGTGTCTTGCTATATTAGGCTGT	2069
	ATGGCATG**G**AAGCTTAT	2070
	ATAAGCTT**C**CATGCCAT	2071
Haemophilia A Tyr323Term TATg-TAA	ATATAGCAAGACACTCTGACATTGTTTGGTTTGTCTGACTCCA GATGGCATGGAAGCTTA**T**GTCAAAGTAGACAGCTGTCCAGAG GAACCCCAACTACGAATGAAAAATAATGAAGAAGCG	2072
	CGCTTCTTCATTATTTTTCATTCGTAGTTGGGGTTCCTCTGGA CAGCTGTCTACTTTGAC**A**TAAGCTTCCATGCCATCTGGAGTCA GACAAACCAAACAATGTCAGAGTGTCTTGCTATAT	2073
	GAAGCTTA**T**GTCAAAGT	2074
	ACTTTGAC**A**TAAGCTTC	2075
Haemophilia A Val326Leu aGTA-CTA	AAGACACTCTGACATTGTTTGGTTTGTCTGACTCCAGATGGCA TGGAAGCTTATGTCAAA**G**TAGACAGCTGTCCAGAGGAACCCC AACTACGAATGAAAAATAATGAAGAAGCGGAAGACT	2076
	AGTCTTCCGCTTCTTCATTATTTTTCATTCGTAGTTGGGGTTC CTCTGGACAGCTGTCTA**C**TTTGACATAAGCTTCCATGCCATCT GGAGTCAGACAAACCAAACAATGTCAGAGTGTCTT	2077
	ATGTCAAA**G**TAGACAGC	2078
	GCTGTCTA**C**TTTGACAT	2079
Haemophilia A Cys329Arg cTGT-CGT	TGACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTT ATGTCAAAGTAGACAGC**T**GTCCAGAGGAACCCCAACTACGAA TGAAAAATAATGAAGAAGCGGAAGACTATGATGATG	2080
	CATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTCGTAGT TGGGGTTCCTCTGGAC**A**GCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAAACAATGTCA	2081
	TAGACAGC**T**GTCCAGAG	2082
	CTCTGGAC**A**GCTGTCTA	2083
Haemophilia A Cys329Tyr TGT-TAT	GACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTTA TGTCAAAGTAGACAGCT**G**TCCAGAGGAACCCCAACTACGAAT GAAAAATAATGAAGAAGCGGAAGACTATGATGATGA	2084
	TCATCATCATAGTCTTCCGCTTCTTCATTATTTTTCATTCGTAG TTGGGGTTCCTCTGGA**C**AGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAAACAATGTC	2085
	AGACAGCT**G**TCCAGAGG	2086
	CCTCTGGA**C**AGCTGTCT	2087
Haemophilia A Arg336Term aCGA-TGA	ACTCCAGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT CCAGAGGAACCCCAACTA**C**GAATGAAAAATAATGAAGAAGCG GAAGACTATGATGATGATCTTACTGATTCTGAAATGG	2088

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCATTTCAGAATCAGTAAGATCATCATCATAGTCTTCCGCTTC TTCATTATTTTTCATTC**G**TAGTTGGGGTTCCTCTGGACAGCTG TCTACTTTGACATAAGCTTCCATGCCATCTGGAGT	2089
	CCCAACTA**C**GAATGAAA	2090
	TTTCATTC**G**TAGTTGGG	2091
Haemophilia A Arg372Cys tCGC-TGC	GATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTC CTTCCTTTATCCAAATT**C**GCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGG	2092
	CCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGATG CTTCTTGGCAACTGAGC**G**AATTTGGATAAAGGAAGGAGAGTT GTCATCATCAAACCTGACCACATCCATTTCAGAATC	2093
	TCCAAATT**C**GCTCAGTT	2094
	AACTGAGC**G**AATTTGGA	2095
Haemophilia A Arg372His CGC-CAC	ATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCC TTCCTTTATCCAAATTC**G**CTCAGTTGCCAAGAAGCATCCTAAA ACTTGGGTACATTACATTGCTGCTGAAGAGGAGGA	2096
	TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAG**C**GAATTTGGATAAAGGAAGGAGAGT TGTCATCATCAAACCTGACCACATCCATTTCAGAAT	2097
	CCAAATTC**G**CTCAGTTG	2098
	CAACTGAG**C**GAATTTGG	2099
Haemophilia A Ser373Leu TCA-TTA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT**C**AGTTGCCAAGAAGCATCCTAAAACT TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2100
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT**G**AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG	2101
	AATTCGCT**C**AGTTGCCA	2102
	TGGCAACT**G**AGCGAATT	2103
Haemophilia A Ser373Pro cTCA-CCA	TCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTT CCTTTATCCAAATTCGC**T**CAGTTGCCAAGAAGCATCCTAAAAC TTGGGTACATTACATTGCTGCTGAAGAGGAGGACT	2104
	AGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGG ATGCTTCTTGGCAACTG**A**GCGAATTTGGATAAAGGAAGGAGA GTTGTCATCATCAAACCTGACCACATCCATTTCAGA	2105
	AAATTCGC**T**CAGTTGCC	2106
	GGCAACTG**A**GCGAATTT	2107
Haemophilia A Ser373Term TCA-TAA	CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT**C**AGTTGCCAAGAAGCATCCTAAAACT TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG	2108

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT**G**AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG	2109
	AATTCGCT**C**AGTTGCCA	2110
	TGGCAACT**G**AGCGAATT	2111
Haemophilia A Ile386Phe cATT-TTT	CCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTA AAACTTGGGTACATTAC**A**TTGCTGCTGAAGAGGAGGACTGGG ACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGT	2112
	ACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCAG TCCTCCTCTTCAGCAGCAA**T**GTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGG	2113
	TACATTAC**A**TTGCTGCT	2114
	AGCAGCAA**T**GTAATGTA	2115
Haemophilia A Ile386Ser ATT-AGT	CTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACA**T**TGCTGCTGAAGAGGAGGACTGGGA CTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGTA	2116
	TACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCA GTCCTCCTCTTCAGCAGCA**A**TGTAATGTACCCAAGTTTTAGGA TGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAG	2117
	ACATTACA**T**TGCTGCTG	2118
	CAGCAGCA**A**TGTAATGT	2119
Haemophilia A Glu390Gly GAG-GGG	AAATTCGCTCAGTTGCCAAGAAGCATCCTAAAACTTGGGTACA TTACATTGCTGCTGAAG**A**GGAGGACTGGGACTATGCTCCCTT AGTCCTCGCCCCCGATGACAGGTAAGCACTTTTTGA	2120
	TCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGACTAAGGGA GCATAGTCCCAGTCCTCC**T**CTTCAGCAGCAATGTAATGTACC CAAGTTTTAGGATGCTTCTTGGCAACTGAGCGAATTT	2121
	TGCTGAAG**A**GGAGGACT	2122
	AGTCCTCC**T**CTTCAGCA	2123
Haemophilia A Trp393Gly cTGG-GGG	TCAGTTGCCAAGAAGCATCCTAAAACTTGGGTACATTACATTG CTGCTGAAGAGGAGGAC**T**GGGACTATGCTCCCTTAGTCCTCG CCCCCGATGACAGGTAAGCACTTTTTGACTATTGGT	2124
	ACCAATAGTCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGA CTAAGGGAGCATAGTCCC**A**GTCCTCCTCTTCAGCAGCAATGT AATGTACCCAAGTTTTAGGATGCTTCTTGGCAACTGA	2125
	AGGAGGAC**T**GGGACTAT	2126
	ATAGTCCC**A**GTCCTCCT	2127
Haemophilia A Lys408Ile AAA-ATA	GCCTACCTAGAATTTTTCTTCCCAACCTCTCATCTTTTTTTCTC TTATACAGAAGTTATA**A**AAGTCAATATTTGAACAATGGCCCTC AGCGGATTGGTAGGAAGTACAAAAAAGTCCGATT	2128

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AATCGGACTTTTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTTCAAATATTGACTT**T**TATAACTTCTGTATAAGAGAAAAAAAGATGAGAGGTTGGGAAGAAAAATTCTAGGTAGGC	2129
	AAGTTATA**A**AAGTCAAT	2130
	ATTGACTT**T**TATAACTT	2131
Haemophilia A Leu412Phe TTGa-TTT	TTTTCTTCCCAACCTCTCATCTTTTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTT**G**AACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAAAAGTCCGATTTATGGCATACACA	2132
	TGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTT**C**AAATATTGACTTTTATAACTTCTGTATAAGAGAAAAAAAGATGAGAGGTTGGGAAGAAAA	2133
	CAATATTT**G**AACAATGG	2134
	CCATTGTT**C**AAATATTG	2135
Haemophilia A Arg418Trp gCGG-TGG	TCATCTTTTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAG**C**GGATTGGTAGGAAGTACAAAAAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGA	2136
	TCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTACCAATCC**G**CTGAGGGCCATTGTTCAAATATTGACTTTTATAACTTCTGTATAAGAGAAAAAAAGATGA	2137
	GCCCTCAG**C**GGATTGGT	2138
	ACCAATCC**G**CTGAGGGC	2139
Haemophilia A Gly420Val GGT-GTT	TTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTG**G**TAGGAAGTACAAAAAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTCGTGA	2140
	TCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTA**C**CAATCCGCTGAGGGCCATTGTTCAAATATTGACTTTTATAACTTCTGTATAAGAGAAAAA	2141
	GCGGATTG**G**TAGGAAGT	2142
	ACTTCCTA**C**CAATCCGC	2143
Haemophilia A Lys425Arg AAA-AGA	GAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAA**A**AGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA	2144
	TCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACT**T**TTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTTCAAATATTGACTTTTATAACTTC	2145
	GTACAAAA**A**AGTCCGAT	2146
	ATCGGACT**T**TTTTGTAC	2147
Haemophilia A Arg427Term cCGA-TGA	TATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAAAAGTC**C**GATTTATGGCATACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAG	2148

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATC TGTGTATGCCATAAATC**G**GACTTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATA	2149
	AAAAAGTC**C**GATTTATG	2150
	CATAAATC**G**GACTTTTT	2151
Haemophilia A Tyr431Asn aTAC-AAC	TATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAA AAAGTCCGATTTATGGCA**T**ACACAGATGAAACCTTTAAGACTC GTGAAGCTATTCAGCATGAATCAGGAATCTTGGGAC	2152
	GTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACGAGTCTT AAAGGTTTCATCTGTGT**A**TGCCATAAATCGGACTTTTTTGTAC TTCCTACCAATCCGCTGAGGGCCATTGTTCAAATA	2153
	TTATGGCA**T**ACACAGAT	2154
	ATCTGTGT**A**TGCCATAA	2155
Haemophilia A Thr435Ile ACC-ATC	GCCCTCAGCGGATTGGTAGGAAGTACAAAAAAGTCCGATTTA TGGCATACACAGATGAAA**C**CTTTAAGACTCGTGAAGCTATTCA GCATGAATCAGGAATCTTGGGACCTTTACTTTATGG	2156
	CCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAG CTTCACGAGTCTTAAAG**G**TTTCATCTGTGTATGCCATAAATCG GACTTTTTTGTACTTCCTACCAATCCGCTGAGGGC	2157
	AGATGAAA**C**CTTTAAGA	2158
	TCTTAAAG**G**TTTCATCT	2159
Haemophilia A Pro451Leu CCT-CTT	ACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA ATCAGGAATCTTGGGAC**C**TTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTC	2160
	GACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAA CTTCCCCATAAAGTAAA**G**GTCCCAAGATTCCTGATTCATGCTG AATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT	2161
	CTTGGGAC**C**TTTACTTT	2162
	AAAGTAAA**G**GTCCCAAG	2163
Haemophilia A Pro451Thr aCCT-ACT	TACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATG AATCAGGAATCTTGGGA**C**CTTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGT	2164
	ACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACT TCCCCATAAAGTAAAG**G**TCCCAAGATTCCTGATTCATGCTGAA TAGCTTCACGAGTCTTAAAGGTTTCATCTGTGTA	2165
	TCTTGGGA**C**CTTTACTT	2166
	AAGTAAAG**G**TCCCAAGA	2167
Haemophilia A Gly455Arg tGGG-AGG	ACCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCT TGGGACCTTTACTTTAT**G**GGGAAGTTGGAGACACACTGTTGG TAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGA	2168

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACTTCCC**C**ATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGGT	2169
	TACTTTATG**G**GGGAAGTT	2170
	AACTTCCC**C**ATAAAGTA	2171
Haemophilia A Gly455Glu GGG-GAG	CCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATG**G**GGAAGTTGGAGACACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGAA	2172
	TTCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACTTCC**C**CATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGG	2173
	ACTTTATG**G**GGAAGTTG	2174
	CAACTTCC**C**CATAAAGT	2175
Haemophilia A Asp459Asn aGAC-AAC	CGTGAAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGGAAGTTGGA**G**ACACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGAAAAAGTCTGGAG	2176
	CTCCAGACTTTTTCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGT**C**TCCAACTTCCCCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAGCTTCACG	2177
	AAGTTGGA**G**ACACACTG	2178
	CAGTGTGT**C**TCCAACTT	2179
Haemophilia A Phe465Cys TTT-TGT	TGTTGATCCTAGTCGTTTTAGGATTTGATCTTAGATCTCGCTTATACTTTCAGATTATAT**T**TAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCC	2180
	GGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTA**A**ATATAATCTGAAAGTATAAGCGAGATCTAAGATCAAATCCTAAAACGACTAGGATCAACA	2181
	GATTATAT**T**TAAGAATC	2182
	GATTCTTA**A**ATATAATC	2183
Haemophilia A Ala469Gly GCA-GGA	TCGTTTTAGGATTTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAG**C**AAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAG	2184
	CTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTT**G**CTTGATTCTTAAATATAATCTGAAAGTATAAGCGAGATCTAAGATCAAATCCTAAAACGA	2185
	GAATCAAG**C**AAGCAGAC	2186
	GTCTGCTT**G**CTTGATTC	2187
Haemophilia A Arg471Gly cAGA-GGA	TTAGGATTTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAGCAAGC**A**GACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAGGAGAT	2188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAAGCGAGATCTAAGATCAAATCCTAA	2189
	AAGCAAGCAGACCATAT	2190
	ATATGGTCTGCTTGCTT	2191
Haemophilia A Tyr473Cys TAT-TGT	TTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAGGAGATTACCAAA	2192
	TTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAAGCGAGATCTAAGATCAA	2193
	CAGACCATATAACATCT	2194
	AGATGTTATATGGTCTG	2195
Haemophilia A Tyr473His aTAT-CAT	TTTGATCTTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAGGAGATTACCAA	2196
	TTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAAGCGAGATCTAAGATCAAA	2197
	GCAGACCATATAACATC	2198
	GATGTTATATGGTCTGC	2199
Haemophilia A Ile475Thr ATC-ACC	TTAGATCTCGCTTATACTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAGGAGATTACCAAAAGGTAA	2200
	TTACCTTTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAAGCGAGATCTAA	2201
	ATATAACATCTACCCTC	2202
	GAGGGTAGATGTTATAT	2203
Haemophilia A Gly479Arg cGGA-AGA	TTATACTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTATTCAAGGAGATTACCAAAAGGTAAATATTCCCTCG	2204
	CGAGGGAATATTTACCTTTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAAGTATAA	2205
	ACCCTCACGGAATCACT	2206
	AGTGATTCCGTGAGGGT	2207
Haemophilia A Thr522Ser aACT-TCT	CCAATTCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAG	2208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTCTCTCCATATTAACGAAACTAGAGTAATAGCGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATATTTGAATATTTCTCCTGGCAGAATTGG	2209
	ATGGGCCAACTAAATCA	2210
	TGATTTAGTTGGCCCAT	2211
Haemophilia A Asp525Asn aGAT-AAT	CCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTT	2212
	AAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATATTTGAATATTTCTCCTGG	2213
	CTAAATCAGATCCTCGG	2214
	CCGAGGATCTGATTTAG	2215
Haemophilia A Arg527Trp tCGG-TGG	GAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGAC	2216
	GTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATATTTGAATATTTC	2217
	CAGATCCTCGGTGCCTG	2218
	CAGGCACCGAGGATCTG	2219
Haemophilia A Arg531Cys cCGC-TGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2220
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA	2221
	GCCTGACCCGCTATTAC	2222
	GTAATAGCGGGTCAGGC	2223
Haemophilia A Arg531Gly cCGC-GGC	TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC	2224
	GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA	2225
	GCCTGACCCGCTATTAC	2226
	GTAATAGCGGGTCAGGC	2227
Haemophilia A Arg531His CGC-CAC	ATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCT	2228

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGTCCATTTAT	2229
	CCTGACCCGCTATTACT	2230
	AGTAATAGCGGGTCAGG	2231
Haemophilia A Ser534Pro cTCT-CCT	ACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCT	2232
	AGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT	2233
	GCTATTACTCTAGTTTC	2234
	GAAACTAGAGTAATAGC	2235
Haemophilia A Ser535Gly tAGT-GGT	GTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCT	2236
	AGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCAC	2237
	ATTACTCTAGTTTCGTT	2238
	AACGAAACTAGAGTAAT	2239
Haemophilia A Val537Asp GTT-GAT	TAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGA	2240
	TCTTTGTAGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTA	2241
	TAGTTTCGTTAATATGG	2242
	CCATATTAACGAAACTA	2243
Haemophilia A Arg541Thr AGA-ACA	CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGAATCTGTAGATCA	2244
	TGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTG	2245
	TATGGAGAGAGATCTAG	2246
	CTAGATCTCTCTCCATA	2247
Haemophilia A Asp542Gly GAT-GGT	CTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAAG	2248

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCA ATGAGTCCTGAAGCTAGA**T**CTCTCTCCATATTAACGAAACTAG AGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAG	2249
	GGAGAGAG**A**TCTAGCTT	2250
	AAGCTAGA**T**CTCTCTCC	2251
Haemophilia A Asp542His aGAT-CAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGA**G**ATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA	2252
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAAT GAGTCCTGAAGCTAGAT**C**TCTCTCCATATTAACGAAACTAGAG TAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT	2253
	TGGAGAGA**G**ATCTAGCT	2254
	AGCTAGAT**C**TCTCTCCA	2255
Haemophilia A Asp542Tyr aGAT-TAT	ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGA**G**ATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA	2256
	TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAAT GAGTCCTGAAGCTAGAT**C**TCTCTCCATATTAACGAAACTAGAG TAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT	2257
	TGGAGAGA**G**ATCTAGCT	2258
	AGCTAGAT**C**TCTCTCCA	2259
Haemophilia A Glu557Term aGAA-TAA	GTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCT CTCCTCATCTGCTACAAA**G**AATCTGTAGATCAAAGAGGAAACC AGGTGAGTTCTTGCCTTTCCAAGTGCTGGGTTTCAT	2260
	ATGAAACCCAGCACTTGGAAAGGCAAGAACTCACCTGGTTTC CTCTTTGATCTACAGATT**C**TTTGTAGCAGATGAGGAGAGGGC CAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAC	2261
	GCTACAAA**G**AATCTGTA	2262
	TACAGATT**C**TTTGTAGC	2263
Haemophilia A Ser558Phe TCT-TTT	ATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCC TCATCTGCTACAAAGAAT**C**TGTAGATCAAAGAGGAAACCAGGT GAGTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTC	2264
	GAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACCTGG TTTCCTCTTTGATCTACA**G**ATTCTTTGTAGCAGATGAGGAGAG GGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATAT	2265
	CAAAGAAT**C**TGTAGATC	2266
	GATCTACA**G**ATTCTTTG	2267
Haemophilia A Val559Ala GTA-GCA	TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCA TCTGCTACAAAGAATCTG**T**AGATCAAAGAGGAAACCAGGTGA GTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTCAGT	2268

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACC TGGTTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGA GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCA	2269
	AGAATCTGTAGATCAAA	2270
	TTTGATCTACAGATTCT	2271

EXAMPLE 14
Hemophilia - Factor IX Deficiency

The attached table discloses the correcting oligonucleotide base sequences for the Factor IX oligonucleotides of the invention.

Table 21
Factor IX Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemophilia B Asn2Asp tAAT-GAT	ATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2272
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTT GTTGGCGTTTTCATGATCAAGAAAAACTGAAAT	2273
	AGAGGTATAATTCAGGT	2274
	ACCTGAATTATACCTCT	2275
Haemophilia B Asn2Ile AAT-ATT	TTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAAT CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAA	2276
	TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT TGTTGGCGTTTTCATGATCAAGAAAAACTGAAA	2277
	GAGGTATAATTCAGGTA	2278
	TACCTGAATTATACCTC	2279
Haemophilia B Asn2Tyr tAAT-TAT	ATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA	2280
	TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTT GTTGGCGTTTTCATGATCAAGAAAAACTGAAAT	2281

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGAGGTAT**_A_**ATTCAGGT	2282
	ACCTGAAT**_T_**ATACCTCT	2283
Haemophilia B Ser3Pro tTCA-CCA	TCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAAT**_T_**CAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT	2284
	ACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTG**_A_**ATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGA	2285
	GGTATAAT**_T_**CAGGTAAA	2286
	TTTACCTG**_A_**ATTATACC	2287
Haemophilia B Gly4Asp GGT-GAT	TTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAG**_G_**TAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG	2288
	CTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTA**_C_**CTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAA	2289
	TAATTCAG**_G_**TAAATTGG	2290
	CCAATTTA**_C_**CTGAATTA	2291
Haemophilia B Gly4Ser aGGT-AGT	GTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCA**_G_**GTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTA	2292
	TACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTAC**_C_**TGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAAC	2293
	ATAATTCA**_G_**GTAAATTG	2294
	CAATTTAC**_C_**TGAATTAT	2295
Haemophilia B Lys5Glu tAAA-GAA	TTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGT**_A_**AATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT	2296
	AACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTT**_T_**ACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAA	2297
	ATTCAGGT**_A_**AATTGGAA	2298
	TTCCAATT**_T_**ACCTGAAT	2299
Haemophilia B Glu7Ala GAA-GCA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGG**_A_**AGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2300
	TCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCT**_T_**CCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGAT	2301

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAAATTGGAAGAGTTTG	2302
	CAAACTCTTCCAATTTA	2303
Haemophilia B Glu7Lys gGAA-AAA	GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAG	2304
	CTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATC	2305
	GTAAATTGGAAGAGTTT	2306
	AAACTCTTCCAATTTAC	2307
Haemophilia B Glu7Val GAA-GTA	ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA	2308
	TCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGAT	2309
	TAAATTGGAAGAGTTTG	2310
	CAAACTCTTCCAATTTA	2311
Haemophilia B Glu8Ala GAG-GCG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2312
	GCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCAT	2313
	ATTGGAAGAGTTTGTTC	2314
	GAACAAACTCTTCCAAT	2315
Haemophilia B Glu8Gly GAG-GGG	ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC	2316
	GCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCAT	2317
	ATTGGAAGAGTTTGTTC	2318
	GAACAAACTCTTCCAAT	2319
Haemophilia B Phe9Cys TTT-TGT	AAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACG	2320
	CGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTT	2321

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGAAGAGT**T**TGTTCAAG	2322
	CTTGAACA**A**ACTCTTCC	2323
Haemophilia B Phe9Ile gTTT-ATT	GAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAG**T**TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC	2324
	GTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA**A**CTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTC	2325
	TGGAAGAG**T**TTGTTCAA	2326
	TTGAACAA**A**CTCTTCCA	2327
Haemophilia B Arg(-1)Ser AGGt-AGC	TTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAG**G**TATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA	2328
	TTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATA**C**CTCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGAAATGTAA	2329
	CCAAAGAG**G**TATAATTC	2330
	GAATTATA**C**CTCTTTGG	2331
Haemophilia B Arg(-1)Thr AGG-ACG	TTTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA**G**GTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGA	2332
	TCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATAC**C**TCTTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGAAATGTAAA	2333
	GCCAAAGA**G**GTATAATT	2334
	AATTATAC**C**TCTTTGGC	2335
Haemophilia B Lys(-2)Asn AAGa-AAT	CTTTTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAA**G**AGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATG	2336
	CATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCT**C**TTTGGCCGATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGAAATGTAAAAG	2337
	CGGCCAAA**G**AGGTATAA	2338
	TTATACCT**C**TTTGGCCG	2339
Haemophilia B Arg(-4)Gln CGG-CAG	AATTATTCTTTTACATTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATC**G**GCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2340
	TCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGC**C**GATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGAAATGTAAAAGAATAATT	2341

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGAATC**G**GCCAAAGA	2342
	TCTTTGGC**C**GATTCAGA	2343
Haemophilia B Arg(-4)Leu CGG-CTG	AATTATTCTTTTACATTTCAGTTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC**G**GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGA	2344
	TCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC**C**GATTCAGAATTTTGTTGGCGTTTTCA TGATCAAGAAAAACTGAAATGTAAAAGAATAATT	2345
	TCTGAATC**G**GCCAAAGA	2346
	TCTTTGGC**C**GATTCAGA	2347
Haemophilia B Arg(-4)Trp tCGG-TGG	GAATTATTCTTTTACATTTCAGTTTTTCTTGATCATGAAAACGC CAACAAAATTCTGAAT**C**GGCCAAAGAGGTATAATTCAGGTAAA TTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAG	2348
	CTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGA ATTATACCTCTTTGGCC**G**ATTCAGAATTTTGTTGGCGTTTTCAT GATCAAGAAAAACTGAAATGTAAAAGAATAATTC	2349
	TTCTGAAT**C**GGCCAAAG	2350
	CTTTGGCC**G**ATTCAGAA	2351
Haemophilia B Gln11Term tCAA-TAA	GCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTA AATTGGAAGAGTTTGTT**C**AAGGGAACCTTGAGAGAGAATGTAT GGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAG	2352
	CTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCT CTCTCAAGGTTCCCTT**G**AACAAACTCTTCCAATTTACCTGAAT TATACCTCTTTGGCCGATTCAGAATTTTGTTGGC	2353
	AGTTTGTT**C**AAGGGAAC	2354
	GTTCCCTT**G**AACAAACT	2355
Haemophilia B Gly12Ala GGG-GCG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAAG**G**GAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTT	2356
	AAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTC**C**CTTGAACAAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTCAGAATTTTGT	2357
	TGTTCAAG**G**GAACCTTG	2358
	CAAGGTTC**C**CTTGAACA	2359
Haemophilia B Gly12Arg aGGG-AGG	AACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAA**G**GGAACCTTGAGAGAGAATGTATGG AAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTT	2360
	AAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACAT TCTCTCTCAAGGTTCC**C**TTGAACAAACTCTTCCAATTTACCTG AATTATACCTCTTTGGCCGATTCAGAATTTTGTT	2361

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGTTCAA**G**GGAACCTT	2362
	AAGGTTCC**C**TTGAACAA	2363
Haemophilia B Gly12Glu GGG-GAG	ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAG**G**GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTT	2364
	AAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTC**C**CTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTTTGT	2365
	TGTTCAAG**G**GAACCTTG	2366
	CAAGGTTC**C**CTTGAACA	2367
Haemophilia B Glu17Gln aGAA-CAA	CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGA**G**AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAA	2368
	TTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATT**C**TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG	2369
	TTGAGAGA**G**AATGTATG	2370
	CATACATT**C**TCTCTCAA	2371
Haemophilia B Glu17Lys aGAA-AAA	CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGA**G**AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAA	2372
	TTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATT**C**TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG	2373
	TTGAGAGA**G**AATGTATG	2374
	CATACATT**C**TCTCTCAA	2375
Haemophilia B Cys18Arg aTGT-CGT	CCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAA**T**GTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAA	2376
	TTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATAC**A**TTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGG	2377
	AGAGAGAA**T**GTATGGAA	2378
	TTCCATAC**A**TTCTCTCT	2379
Haemophilia B Cys18Tyr TGT-TAT	CAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAAT**G**TATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAAC	2380
	GTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATA**C**ATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTG	2381

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGAGAAT**G**TATGGAAG	2382
	CTTCCATA**C**ATTCTCTC	2383
Haemophilia B Glu20Val GAA-GTA	GGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGG**A**AGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAG	2384
	CTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCT**T**CCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATACC	2385
	ATGTATGG**A**AGAAAAGT	2386
	ACTTTTCT**T**CCATACAT	2387
Haemophilia B Glu21Lys aGAA-AAA	TATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA**G**AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTA	2388
	TACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTT**C**TTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGAATTATA	2389
	GTATGGAA**G**AAAAGTGT	2390
	ACACTTTT**C**TTCCATAC	2391
Haemophilia B Cys23Arg gTGT-CGT	TCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAG**T**GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCA	2392
	TGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTAC**A**CTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTGA	2393
	AAGAAAAG**T**GTAGTTTT	2394
	AAAACTAC**A**CTTTTCTT	2395
Haemophilia B Cys23Tyr TGT-TAT	CAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT**G**TAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCAC	2396
	GTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCAAAACTA**C**ACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATTTACCTG	2397
	AGAAAAGT**G**TAGTTTTG	2398
	CAAAACTA**C**ACTTTTCT	2399
Haemophilia B Phe25Ser TTT-TCT	AATTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT**T**TGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATA	2400
	TATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTCGTGCTTCTTCA**A**AACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTCCAATT	2401

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTGTAGTT**T**TGAAGAAG	2402
	CTTCTTCA**A**AACTACAC	2403
Haemophilia B Glu26Gln tGAA-CAA	TTGGAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATG GAAGAAAAGTGTAGTTTT**G**AAGAAGCACGAGAAGTTTTTGAAA ACACTGAAAGAACAGTGAGTATTTCCACATAATACC	2404
	GGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAA ACTTCTCGTGCTTCTT**C**AAAACTACACTTTTCTTCCATACATTC TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAA	2405
	GTAGTTTT**G**AAGAAGCA	2406
	TGCTTCTT**C**AAAACTAC	2407
Haemophilia B Glu27Ala GAA-GCA	AAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAG**A**AGCACGAGAAGTTTTTGAAAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2408
	GAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT CAAAAACTTCTCGTGCT**T**CTTCAAAACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2409
	TTTTGAAG**A**AGCACGAG	2410
	CTCGTGCT**T**CTTCAAAA	2411
Haemophilia B Glu27Asp GAAg-GAC	AGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGA AAAGTGTAGTTTTGAAGA**A**GCACGAGAAGTTTTTGAAAACACT GAAAGAACAGTGAGTATTTCCACATAATACCCTTCA	2412
	TGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTT TCAAAAACTTCTCGTGC**T**TCTTCAAAACTACACTTTTCTTCCAT ACATTCTCTCTCAAGGTTCCCTTGAACAAACTCT	2413
	TTTGAAGA**A**GCACGAGA	2414
	TCTCGTGC**T**TCTTCAAA	2415
Haemophilia B Glu27Lys aGAA-AAA	GAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA GAAAAGTGTAGTTTTGAA**G**AAGCACGAGAAGTTTTTGAAAACA CTGAAAGAACAGTGAGTATTTCCACATAATACCCTT	2416
	AAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTC AAAAACTTCTCGTGCTT**C**TTCAAAACTACACTTTTCTTCCATAC ATTCTCTCTCAAGGTTCCCTTGAACAAACTCTTC	2417
	GTTTTGAA**G**AAGCACGA	2418
	TCGTGCTT**C**TTCAAAAC	2419
Haemophilia B Glu27Val GAA-GTA	AAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAG**A**AGCACGAGAAGTTTTTGAAAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC	2420
	GAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT CAAAAACTTCTCGTGCT**T**CTTCAAAACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT	2421

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTTGAAG**A**AGCACGAG	2422
	CTCGTGCT**T**CTTCAAAA	2423
Haemophilia B Arg29Gln CGA-CAA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC**G**AGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2424
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCT**C**GTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2425
	AGAAGCAC**G**AGAAGTTT	2426
	AAACTTCT**C**GTGCTTCT	2427
Haemophilia B Arg29Pro CGA-CCA	TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC**G**AGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGC	2428
	GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCT**C**GTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA	2429
	AGAAGCAC**G**AGAAGTTT	2430
	AAACTTCT**C**GTGCTTCT	2431
Haemophilia B Arg29Term aCGA-TGA	TTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCA**C**GAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATG	2432
	CATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTTCTC**G**TGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAA	2433
	AAGAAGCA**C**GAGAAGTT	2434
	AACTTCTC**G**TGCTTCTT	2435
Haemophilia B Glu30Lys aGAA-AAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGA**G**AAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2436
	CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTT**C**TCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2437
	AAGCACGA**G**AAGTTTTT	2438
	AAAAACTT**C**TCGTGCTT	2439
Haemophilia B Glu30Term aGAA-TAA	GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGA**G**AAGTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCAG	2440
	CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACTT**C**TCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC	2441

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAGCACGA**G**AAGTTTTT	2442
	AAAAACTT**C**TCGTGCTT	2443
Haemophilia B Glu33Asp GAAa-GAC	CCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAA**A**AACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCAGAGCATAGAATA	2444
	TATTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTT**T**TCAAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGG	2445
	GTTTTTGA**A**AAACACTGA	2446
	TCAGTGTT**T**TCAAAAAC	2447
Haemophilia B Glu33Term tGAA-TAA	AACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTT**G**AAAACACTGAAAGAACAGTGAGTATTTCCACATAATACCCTTCAGATGCAGAGCATAGAA	2448
	TTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTCAGTGTTTT**C**AAAAACTTCTCGTGCTTCTTCAAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT	2449
	AAGTTTTT**G**AAAACACT	2450
	AGTGTTTT**C**AAAAACTT	2451
Haemophilia B Trp42Term TGG-TAG	CAAAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAGACTGAATTTTT**G**GAAGCAGTATGTTGGTAAGCAATTCATTTTATCCTCTAGCTAATATATGAAACATATGAG	2452
	CTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTTACCAACATACTGCTTC**C**AAAATTCAGTCTATAAAGAATAAAAGAAGACAAATTAACGGTAATATCTAAAGTGTTTTG	2453
	TGAATTTT**G**GAAGCAGT	2454
	ACTGCTTC**C**AAAATTCA	2455
Haemophilia B Lys43Glu gAAG-GAG	AAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAGACTGAATTTTGG**A**AGCAGTATGTTGGTAAGCAATTCATTTTATCCTCTAGCTAATATATGAAACATATGAGAA	2456
	TTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTTACCAACATACTGCT**T**CCAAAATTCAGTCTATAAAGAATAAAAGAAGACAAATTAACGGTAATATCTAAAGTGTTT	2457
	AATTTTGG**A**AGCAGTAT	2458
	ATACTGCT**T**CCAAAATT	2459
Haemophilia B Gln44Term gCAG-TAG	CACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAGACTGAATTTTGGAAG**C**AGTATGTTGGTAAGCAATTCATTTTATCCTCTAGCTAATATATGAAACATATGAGAATTA	2460
	TAATTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTTACCAACATACT**G**CTTCCAAAATTCAGTCTATAAAGAATAAAAGAAGACAAATTAACGGTAATATCTAAAGTG	2461

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTGGAAGCAGTATGTT	2462
	AACATACTGCTTCCAAA	2463
Haemophilia B Asp49Gly GAT-GGT	CCGGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAAC CTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTA AATGGCGGCAGTTGCAAGGATGACATTAATTCCTA	2464
	TAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATG GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAA ATTGAATTGGCACGTAAACTGCTTAGAATGCCCGG	2465
	AGATGGAGATCAGTGTG	2466
	CACACTGATCTCCATCT	2467
Haemophilia B Gln50His CAGt-CAC	GCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATC TCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAA	2468
	TTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAA CATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTA AGAAATTGAATTGGCACGTAAACTGCTTAGAATGC	2469
	GGAGATCAGTGTGAGTC	2470
	GACTCACACTGATCTCC	2471
Haemophilia B Gln50Pro CAG-CCG	GGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTA TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGATGACATTAATTCCTATGA	2472
	TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAA GAAATTGAATTGGCACGTAAACTGCTTAGAATGCC	2473
	TGGAGATCAGTGTGAGT	2474
	ACTCACACTGATCTCCA	2475
Haemophilia B Gln50Term tCAG-TAG	GGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCT ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAA TGGCGGCAGTTGCAAGGATGACATTAATTCCTATG	2476
	CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAG AAATTGAATTGGCACGTAAACTGCTTAGAATGCCC	2477
	ATGGAGATCAGTGTGAG	2478
	CTCACACTGATCTCCAT	2479
Haemophilia B Cys51Arg gTGT-CGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2480
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAAACTGCTTAGAATG	2481

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAGATCAGTGTGAGTCC	2482
	GGACTCACACTGATCTC	2483
Haemophilia B Cys51Ser gTGT-AGT	CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAAT	2484
	ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAAACTGCTTAGAATG	2485
	GAGATCAGTGTGAGTCC	2486
	GGACTCACACTGATCTC	2487
Haemophilia B Cys51Trp TGTg-TGG	TTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGT	2488
	ACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAAACTGCTTAGAA	2489
	GATCAGTGTGAGTCCAA	2490
	TTGGACTCACACTGATC	2491
Haemophilia B Glu52Term tGAG-TAG	TCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT	2492
	AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAAACTGCTTAGA	2493
	ATCAGTGTGAGTCCAAT	2494
	ATTGGACTCACACTGAT	2495
Haemophilia B Pro55Ala tCCA-GCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCT	2496
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAAA	2497
	AGTCCAATCCATGTTTA	2498
	TAAACATGGATTGGACT	2499
Haemophilia B Pro55Arg CCA-CGA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2500
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2501

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCCAATC**C**ATGTTTAA	2502
	TTAAACAT**G**GATTGGAC	2503
Haemophilia B Pro55Gln CCA-CAA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATC**C**ATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2504
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACAT**G**GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2505
	GTCCAATC**C**ATGTTTAA	2506
	TTAAACAT**G**GATTGGAC	2507
Haemophilia B Pro55Leu CCA-CTA	TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATC**C**ATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTT	2508
	AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACAT**G**GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA	2509
	GTCCAATC**C**ATGTTTAA	2510
	TTAAACAT**G**GATTGGAC	2511
Haemophilia B Pro55Ser tCCA-TCA	TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAAT**C**CATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCT	2512
	AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATG**G**ATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGTAAA	2513
	AGTCCAAT**C**CATGTTTA	2514
	TAAACATG**G**ATTGGACT	2515
Haemophilia B Cys56Arg aTGT-CGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCA**T**GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2516
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC**A**TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2517
	CCAATCCA**T**GTTTAAAT	2518
	ATTTAAAC**A**TGGATTGG	2519
Haemophilia B Cys56Ser aTGT-AGT	ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCA**T**GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG	2520
	CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC**A**TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT	2521

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAATCCA**T**GTTTAAAT	2522
	ATTTAAAC**A**TGGATTGG	2523
Haemophilia B Cys56Ser TGT-TCT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCAT**G**TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2524
	CCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAA**C**ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2525
	CAATCCAT**G**TTTAAATG	2526
	CATTTAAA**C**ATGGATTG	2527
Haemophilia B Cys56Tyr TGT-TAT	CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCAT**G**TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG	2528
	CCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAA**C**ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG	2529
	CAATCCAT**G**TTTAAATG	2530
	CATTTAAA**C**ATGGATTG	2531
Haemophilia B Asn58Lys AATg-AAG	ATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAA**T**GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAA	2532
	TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCC**A**TTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAAT	2533
	TGTTTAAA**T**GGCGGCAG	2534
	CTGCCGCC**A**TTTAAACA	2535
Haemophilia B Gly59Asp GGC-GAC	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATG**G**CGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG	2536
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCG**C**CATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2537
	TTTAAATG**G**CGGCAGTT	2538
	AACTGCCG**C**CATTTAAA	2539
Haemophilia B Gly59Val GGC-GTC	TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATG**G**CGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG	2540
	CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCG**C**CATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA	2541

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTTAAATG**G**CGGCAGTT	2542
	AACTGCCG**C**CATTTAAA	2543
Haemophilia B Gly59Ser tGGC-AGC	TTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT**G**GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAG	2544
	CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGC**C**ATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATTGAA	2545
	GTTTAAAT**G**GCGGCAGT	2546
	ACTGCCGC**C**ATTTAAAC	2547
Haemophilia B Gly60Ser cGGC-AGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGC**G**GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2548
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGC**C**GCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2549
	TAAATGGC**G**GCAGTTGC	2550
	GCAACTGC**C**GCCATTTA	2551
Haemophilia B Gly60Cys cGGC-TGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGC**G**GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2552
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGC**C**GCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2553
	TAAATGGC**G**GCAGTTGC	2554
	GCAACTGC**C**GCCATTTA	2555
Haemophilia B Gly60Asp GGC-GAC	ATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG**G**CAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAA	2556
	TTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTG**C**CGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAAT	2557
	AAATGGCG**G**CAGTTGCA	2558
	TGCAACTG**C**CGCCATTT	2559
Haemophilia B Gly60Arg cGGC-CGC	AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGC**G**GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA	2560
	TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGC**C**GCCATTTAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAAATT	2561

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAAATGGC**G**GCAGTTGC	2562
	GCAACTGC**C**GCCATTTA	2563
Haemophilia B Cys62Tyr TGC-TAC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTT**G**CAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2564
	CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTG**C**AACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA	2565
	CGGCAGTT**G**CAAGGATG	2566
	CATCCTTG**C**AACTGCCG	2567
Haemophilia B Cys62Ser TGC-TCC	TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTT**G**CAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG	2568
	CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTG**C**AACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA	2569
	CGGCAGTT**G**CAAGGATG	2570
	CATCCTTG**C**AACTGCCG	2571
Haemophilia B Cys62Term TGCa-TGA	AACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGT TTAAATGGCGGCAGTTG**C**AAGGATGACATTAATTCCTATGAAT GTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGT	2572
	ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTT**G**CAACTGCCGCCATTTAAACATGGAT TGGACTCACACTGATCTCCATCTTTGAGATAGGTT	2573
	GGCAGTTG**C**AAGGATGA	2574
	TCATCCTT**G**CAACTGCC	2575
Haemophilia B Asp64Glu GATg-GAG	TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGA**T**GACATTAATTCCTATGAATGTTGG TGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTA	2576
	TAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTC**A**TCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGA	2577
	TGCAAGGA**T**GACATTAA	2578
	TTAATGTC**A**TCCTTGCA	2579
Haemophilia B Asp64Gly GAT-GGT	ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAA TGGCGGCAGTTGCAAGG**A**TGACATTAATTCCTATGAATGTTG GTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATT	2580
	AATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATT CATAGGAATTAATGTCA**T**CCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGAT	2581

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGCAAGGATGACATTA	2582
	TAATGTCATCCTTGCAA	2583
Haemophilia B Asp64Asn gGAT-AAT	TATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAA ATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTG GTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAAT	2584
	ATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTC ATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACAT GGATTGGACTCACACTGATCTCCATCTTTGAGATA	2585
	GTTGCAAGGATGACATT	2586
	AATGTCATCCTTGCAAC	2587
Haemophilia B Ile66Ser ATT-AGT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAA	2588
	TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2589
	GGATGACATTAATTCCT	2590
	AGGAATTAATGTCATCC	2591
Haemophilia B Ile66Thr ATT-ACT	AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAA	2592
	TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT	2593
	GGATGACATTAATTCCT	2594
	AGGAATTAATGTCATCC	2595
Haemophilia B Asn67Lys AATt-AAA	TGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAG TTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTT GGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAA	2596
	TTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGAC ACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCC ATTTAAACATGGATTGGACTCACACTGATCTCCA	2597
	GACATTAATTCCTATGA	2598
	TCATAGGAATTAATGTC	2599
Haemophilia B Tyr69Cys TAT-TGT	ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATT TGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATT	2600
	AATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAA GGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTG CCGCCATTTAAACATGGATTGGACTCACACTGAT	2601

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATTCCTATGAATGTT	2602
	AACATTCATAGGAATTA	2603
Haemophilia B Cys71Term TGTt-TGA	TGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAA	2604
	TTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCA	2605
	TATGAATGTTGGTGTCC	2606
	GGACACCAACATTCATA	2607
Haemophilia B Cys71Ser TGT-TCT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGA	2608
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCAC	2609
	CTATGAATGTTGGTGTC	2610
	GACACCAACATTCATAG	2611
Haemophilia B Cys71Tyr TGT-TAT	GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGA	2612
	TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCAC	2613
	CTATGAATGTTGGTGTC	2614
	GACACCAACATTCATAG	2615
Haemophilia B Cys71Ser aTGT-AGT	TGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTG	2616
	CAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA	2617
	CCTATGAATGTTGGTGT	2618
	ACACCAACATTCATAGG	2619
Haemophilia B Trp72Arg tTGG-AGG	GAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAAT	2620
	ATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTC	2621

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGAATGT**T**GGTGTCCC	2622
	GGGACACC**A**ACATTCAT	2623
Haemophilia B Trp72Term TGGt-TGA	GTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTG**G**TGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATAC	2624
	GTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACA**C**CAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGAC	2625
	GAATGTTG**G**TGTCCCTT	2626
	AAGGGACA**C**CAACATTC	2627
Haemophilia B Cys73Tyr TGT-TAT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT**G**TCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTC	2628
	GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGA**C**ACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGG	2629
	ATGTTGGT**G**TCCCTTTG	2630
	CAAAGGGA**C**ACCAACAT	2631
Haemophilia B Cys73Arg gTGT-CGT	TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG**T**GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACT	2632
	AGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGAC**A**CCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGGA	2633
	AATGTTGG**T**GTCCCTTT	2634
	AAAGGGAC**A**CCAACATT	2635
Haemophilia B Cys73Phe TGT-TTT	CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT**G**TCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTC	2636
	GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGA**C**ACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTGG	2637
	ATGTTGGT**G**TCCCTTTG	2638
	CAAAGGGA**C**ACCAACAT	2639
Haemophilia B Cys73Term TGTc-TGA	CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTG**T**CCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCA	2640
	TGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGG**A**CACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATTG	2641
	TGTTGGTG**T**CCCTTTGG	2642

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAAAGGGACACCAACA	2643
Haemophilia B Gly76Val GGA-GTA	GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCATGGTTCAA	2644
	TTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC	2645
	TCCCTTTGGATTTGAAG	2646
	CTTCAAATCCAAAGGGA	2647
Haemophilia B Gly76Arg tGGA-AGA	TGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCATGGTTCA	2648
	TGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA	2649
	GTCCCTTTGGATTTGAA	2650
	TTCAAATCCAAAGGGAC	2651
Haemophilia B Phe77Cys TTT-TGT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCATGGTTCAAAGT	2652
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2653
	CTTTGGATTTGAAGGAA	2654
	TTCCTTCAAATCCAAAG	2655
Haemophilia B Phe77Ser TTT-TCT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCATGGTTCAAAGT	2656
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2657
	CTTTGGATTTGAAGGAA	2658
	TTCCTTCAAATCCAAAG	2659
Haemophilia B Phe77Tyr TTT-TAT	TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTGAATACTCATGGTTCAAAGT	2660
	ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTA	2661
	CTTTGGATTTGAAGGAA	2662

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTCCTTCA**A**ATCCAAAG	2663
Haemophilia B Glu78Lys tGAA-AAA	AATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT GGTGTCCCTTTGGATTT**G**AAGGAAAGAACTGTGAATTAGGTAA GTAACTATTTTTTGAATACTCATGGTTCAAAGTTT	2664
	AAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAAT TCACAGTTCTTTCCTT**C**AAATCCAAAGGGACACCAACATTCAT AGGAATTAATGTCATCCTTGCAACTGCCGCCATT	2665
	TTGGATTT**G**AAGGAAAG	2666
	CTTTCCTT**C**AAATCCAA	2667
Haemophilia B Gly79Val GGA-GTA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAG**G**AAAGAACTGTGAATTAGGTAAGTA ACTATTTTTTGAATACTCATGGTTCAAAGTTTCCCT	2668
	AGGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTT**C**CTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2669
	ATTTGAAG**G**AAAGAACT	2670
	AGTTCTTT**C**CTTCAAAT	2671
Haemophilia B Gly79Arg aGGA-AGA	GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCCTTTGGATTTGAA**G**GAAAGAACTGTGAATTAGGTAAGT AACTATTTTTTGAATACTCATGGTTCAAAGTTTCCC	2672
	GGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACC TAATTCACAGTTCTTTC**C**TTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCC	2673
	GATTTGAA**G**GAAAGAAC	2674
	GTTCTTTC**C**TTCAAATC	2675
Haemophilia B Gly79Glu GGA-GAA	GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAG**G**AAAGAACTGTGAATTAGGTAAGTA ACTATTTTTTGAATACTCATGGTTCAAAGTTTCCCT	2676
	AGGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTT**C**CTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC	2677
	ATTTGAAG**G**AAAGAACT	2678
	AGTTCTTT**C**CTTCAAAT	2679
Haemophilia B Cys88Ser TGT-TCT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACAT**G**TAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2680
	ACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATC TGCCATTCTTAATGTTA**C**ATGTTACATCTAAAAGAAGCAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA	2681
	TGTAACAT**G**TAACATTA	2682

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TAATGTTA**C**ATGTTACA	2683
Haemophilia B Cys88Phe TGT-TTT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATG**G**TAACATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2684
	ACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCATTCTTAATGTTA**C**ATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGCATCATTTAACATGCATTTCTAA	2685
	TGTAACAT**G**TAACATTA	2686
	TAATGTTA**C**ATGTTACA	2687
Haemophilia B Cys88Arg aTGT-CGT	TTTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACA**T**GTAACATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGG	2688
	CCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCATTCTTAATGTTAC**A**TGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGCATCATTTAACATGCATTTCTAAA	2689
	ATGTAACA**T**GTAACATT	2690
	AATGTTAC**A**TGTTACAT	2691
Haemophilia B Cys88Tyr TGT-TAT	TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACAT**G**TAACATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT	2692
	ACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCATTCTTAATGTTA**C**ATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGCATCATTTAACATGCATTTCTAA	2693
	TGTAACAT**G**TAACATTA	2694
	TAATGTTA**C**ATGTTACA	2695
Haemophilia B Ile90Thr ATT-ACT	ATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACA**T**TAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTC	2696
	GAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCATTCTTA**A**TGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGCATCATTTAACATGCAT	2697
	ATGTAACA**T**TAAGAATG	2698
	CATTCTTA**A**TGTTACAT	2699
Haemophilia B Asn92His gAAT-CAT	TGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAG**A**ATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTA	2700
	TACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCAT**T**CTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGCATCATTTAACA	2701
	ACATTAAG**A**ATGGCAGA	2702

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TCTGCCAT**T**CTTAATGT	2703
Haemophilia B Asn92Lys AATg-AAA	TTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAA CATGTAACATTAAGAA**T**GGCAGATGCGAGCAGTTTTGTAAAAA TAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT	2704
	AGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAA AACTGCTCGCATCTGCC**A**TTCTTAATGTTACATGTTACATCTA AAAGAAGCAAAATAGACAGTAACAGCATCATTTAA	2705
	ATTAAGAA**T**GGCAGATG	2706
	CATCTGCC**A**TTCTTAAT	2707
Haemophilia B Gly93Asp GGC-GAC	AAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACA TGTAACATTAAGAATG**G**CAGATGCGAGCAGTTTTGTAAAAATA GTGCTGATAACAAGGTGGTTTGCTCCTGTACTGA	2708
	TCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTAC AAAACTGCTCGCATCTG**C**CATTCTTAATGTTACATGTTACATCT AAAAGAAGCAAAATAGACAGTAACAGCATCATTT	2709
	TAAGAATG**G**CAGATGCG	2710
	CGCATCTG**C**CATTCTTA	2711
Haemophilia B Gly93Ser tGGC-AGC	TAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAAC ATGTAACATTAAGAAT**G**GCAGATGCGAGCAGTTTTGTAAAAAT AGTGCTGATAACAAGGTGGTTTGCTCCTGTACTG	2712
	CAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACA AAACTGCTCGCATCTGC**C**ATTCTTAATGTTACATGTTACATCTA AAAGAAGCAAAATAGACAGTAACAGCATCATTTA	2713
	TTAAGAAT**G**GCAGATGC	2714
	GCATCTGC**C**ATTCTTAA	2715
Haemophilia B Arg94Ser AGAt-AGT	GATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTA ACATTAAGAATGGCAG**A**TGCGAGCAGTTTTGTAAAAATAGTGC TGATAACAAGGTGGTTTGCTCCTGTACTGAGGGA	2716
	TCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTT TTACAAAACTGCTCGCA**T**CTGCCATTCTTAATGTTACATGTTAC ATCTAAAAGAAGCAAAATAGACAGTAACAGCATC	2717
	AATGGCAG**A**TGCGAGCA	2718
	TGCTCGCA**T**CTGCCATT	2719
Haemophilia B Cys95Tyr TGC-TAC	TGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAAC ATTAAGAATGGCAGAT**G**CGAGCAGTTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATA	2720
	TATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTAT TTTTACAAAACTGCTCG**C**ATCTGCCATTCTTAATGTTACATGTT ACATCTAAAAGAAGCAAAATAGACAGTAACAGCA	2721
	TGGCAGAT**G**CGAGCAGT	2722

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGCTCG**C**ATCTGCCA	2723
Haemophilia B Cys95Trp TGCg-TGG	GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATG**C**GAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2724
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTC**G**CATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGC	2725
	GGCAGATG**C**GAGCAGTT	2726
	AACTGCTC**G**CATCTGCC	2727
Haemophilia B Cys95Term TGCg-TGA	GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATG**C**GAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT	2728
	ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACTGCTC**G**CATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTAACAGC	2729
	GGCAGATG**C**GAGCAGTT	2730
	AACTGCTC**G**CATCTGCC	2731
Haemophilia B Gln97Pro CAG-CCG	TACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC**A**GTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGATATCGACT	2732
	AGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAAC**T**GCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTA	2733
	ATGCGAGC**A**GTTTTGTA	2734
	TACAAAAC**T**GCTCGCAT	2735
Haemophilia B Gln97Glu gCAG-GAG	TTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG**C**AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGATATCGAC	2736
	GTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTACAAAACT**G**CTCGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGACAGTAA	2737
	GATGCGAG**C**AGTTTTGT	2738
	ACAAAACT**G**CTCGCATC	2739
Haemophilia B Cys99Arg tTGT-CGT	TCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGCAGTTT**T**GTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGATATCGACTTGCAG	2740
	CTGCAAGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTTAC**A**AAACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAATAGA	2741
	AGCAGTTT**T**GTAAAAAT	2742

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATTTTTACAAAACTGCT	2743
Haemophilia B Cys99Tyr TGT-TAT	CTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGC AGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTG GTTTGCTCCTGTACTGAGGGATATCGACTTGCAGA	2744
	TCTGCAAGTCGATATCCCTCAGTACAGGAGCAAACCACCTTG TTATCAGCACTATTTTTACAAAACTGCTCGCATCTGCCATTCTT AATGTTACATGTTACATCTAAAAGAAGCAAAATAG	2745
	GCAGTTTTGTAAAAATA	2746
	TATTTTTACAAAACTGC	2747
Warfarin sensitivity Ala(-10)Thr cGCC-ACC	TTTTTTGCTAAAACTAAAGAATTATTCTTTTACATTTCAGTTTTT CTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTTC	2748
	GAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG ATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGAAA TGTAAAAGAATAATTCTTTAGTTTTAGCAAAAAA	2749
	ATGAAAACGCCAACAAA	2750
	TTTGTTGGCGTTTTCAT	2751
Warfarin sensitivity Ala(-10)Val GCC-GTC	TTTTTGCTAAAACTAAAGAATTATTCTTTTACATTTCAGTTTTTC TTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAG GTATAATTCAGGTAAATTGGAAGAGTTTGTTCA	2752
	TGAACAAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCC GATTCAGAATTTTGTTGGCGTTTTCATGATCAAGAAAAACTGA AATGTAAAAGAATAATTCTTTAGTTTTAGCAAAAA	2753
	TGAAAACGCCAACAAAA	2754
	TTTTGTTGGCGTTTTCA	2755
Haemophilia B Gly(-26)Val GGA-GTA	TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTAC AGGTTTGTTTCCTTTTTTAAAATACATTGAGTATGC	2756
	GCATACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTC AGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCC TGGTGATTCTGCCATGATCATGTTCACGCGCTGCA	2757
	CCTTTTAGGATATCTAC	2758
	GTAGATATCCTAAAAGG	2759
Haemophilia B Leu(-27)Term TTA-TAA	TTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCC TCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATG TACAGGTTTGTTTCCTTTTTTAAAATACATTGAGTA	2760
	TACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTCAGC ACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCCTGG TGATTCTGCCATGATCATGTTCACGCGCTGCATAA	2761
	CTGCCTTTTAGGATATC	2762

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GATATCCTAAAAGGCAG	2763
Haemophilia B Ile(-30)Asn ATC-AAC	TAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGGTTTGTTTCCTTTTTTAAAATA	2764
	TATTTTAAAAAAGGAAACAAACCTGTACATTCAGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTGCCATGATCATGTTCACGCGCTGCATAACCTTTGCTA	2765
	CATCACCATCTGCCTTT	2766
	AAAGGCAGATGGTGATG	2767
Haemophilia B Ile(-40)Phe gATC-TTC	ACTAATCGACCTTACCACTTTCACAATCTGCTAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTG	2768
	CAGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTGCCATGATCATGTTCACGCGCTGCATAACCTTTGCTAGCAGATTGTGAAAGTGGTAAGGTCGATTAGT	2769
	TGAACATGATCATGGCA	2770
	TGCCATGATCATGTTCA	2771
Haemophilia B Arg(-44)His CGC-CAC	ACTTTGGTACAACTAATCGACCTTACCACTTTCACAATCTGCTAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCATCACCATCTGCCTTTTAGGATATCT	2772
	AGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTGCCATGATCATGTTCACGCGCTGCATAACCTTTGCTAGCAGATTGTGAAAGTGGTAAGGTCGATTAGTTGTACCAAAGT	2773
	TATGCAGCGCGTGAACA	2774
	TGTTCACGCGCTGCATA	2775

EXAMPLE 15
Alpha thalassemia - Hemoglobin alpha locus 1

The thalassemia syndromes are a heterogeneous group of inherited anemias characterized by defects in the synthesis of one or more globin chain subunits. For example, beta-thalassemia discussed in Example 6, is caused by a decrease in beta-chain production relative to alpha-chain production; the converse is the case for alpha-thalassemia. The attached table discloses the *correcting oligonucleotide base sequences for the hemoglobin alpha locus 1 oligonucleotides of the* invention.

Table 22
HBA1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Val cATG-GTG	CCCTGGCGCGCTCGCGGCCCGGCACTCTTCTGGTCCCCACA GACTCAGAGAGAACCCACC**A**TGGTGCTGTCTCCTGCCGACA AGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGC	2776
	GCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTTG TCGGCAGGAGACAGCACCA**T**GGTGGGTTCTCTCTGAGTCTGT GGGGACCAGAAGAGTGCCGGGCCGCGAGCGCGCCAGGG	2777
	AACCCACC**A**TGGTGCTG	2778
	CAGCACCA**T**GGTGGGTT	2779
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCC GACAAGACCAACGTCAAGG**C**CGCCTGGGGTAAGGTCGGCGC GCACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2780
	CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCCAGGCG**G**CCTTGACGTTGGTCTTGTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG	2781
	CGTCAAGG**C**CGCCTGGG	2782
	CCCAGGCG**G**CCTTGACG	2783
Haemoglobin variant Gly15Asp GGT-GAT	AGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCA ACGTCAAGGCCGCCTGGG**G**TAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCT	2784
	AGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCC AGCGTGCGCGCCGACCTTA**C**CCCAGGCGGCCTTGACGTTGG TCTTGTCGGCAGGAGACAGCACCATGGTGGGTTCTCTCT	2785
	CGCCTGGG**G**TAAGGTCG	2786
	CGACCTTA**C**CCCAGGCG	2787
Haemoglobin variant Tyr24Cys TAT-TGT	CTGCCGACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTC GGCGCGCACGCTGGCGAGT**A**TGGTGCGGAGGCCCTGGAGA GGTGAGGCTCCCTCCCCTGCTCCGACCCGGGCTCCTCGCC	2788
	GGCGAGGAGCCCGGGTCGGAGCAGGGGAGGGAGCCTCACC TCTCCAGGGCCTCCGCACCA**T**ACTCGCCAGCGTGCGCGCCG ACCTTACCCCAGGCGGCCTTGACGTTGGTCTTGTCGGCAG	2789
	TGGCGAGT**A**TGGTGCGG	2790
	CCGCACCA**T**ACTCGCCA	2791
Haemoglobin variant Glu27Asp GAGg-GAT	GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGA**G**GCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGAC C	2792
	GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGC**C**TCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTC	2793
	GGTGCGGA**G**GCCCTGGA	2794
	TCCAGGGC**C**TCCGCACC	2795

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA**C**GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2796
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGC**G**TTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2797
	CTGACCAA**C**GCCGTGGC	2798
	GCCACGGC**G**TTGGTCAG	2799
Haemoglobin variant Asp74Gly GAC-GGC	AGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACC AACGCCGTGGCGCACGTGG**A**CGACATGCCCAACGCGCTGTC CGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGGA	2800
	TCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGA CAGCGCGTTGGGCATGTCG**T**CCACGTGCGCCACGGCGTTGG TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCT	2801
	GCACGTGG**A**CGACATGC	2802
	GCATGTCG**T**CCACGTGC	2803
Haemoglobin variant Asp74His gGAC-CAC	CAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGAC CAACGCCGTGGCGCACGTG**G**ACGACATGCCCAACGCGCTGT CCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG	2804
	CCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGAC AGCGCGTTGGGCATGTCGT**C**CACGTGCGCCACGGCGTTGGT CAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTG	2805
	CGCACGTG**G**ACGACATG	2806
	CATGTCGT**C**CACGTGCG	2807
Haemoglobin variant Asn78His cAAC-CAC	CACGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGG CGCACGTGGACGACATGCCC**A**ACGCGCTGTCCGCCCTGAGC GACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACT	2808
	AGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCG CTCAGGGCGGACAGCGCGT**T**GGGCATGTCGTCCACGTGCGC CACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCGTG	2809
	ACATGCCC**A**ACGCGCTG	2810
	CAGCGCGT**T**GGGCATGT	2811
Haemoglobin variant His87Tyr gCAC-TAC	ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCT GTCCGCCCTGAGCGACCTG**C**ACGCGCACAAGCTTCGGGTGG ACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGGAGCGA	2812
	TCGCTCCCGGCCCGCCGCTCACCTTGAAGTTGACCGGGTCC ACCCGAAGCTTGTGCGCGT**G**CAGGTCGCTCAGGGCGGACAG CGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT	2813
	GCGACCTG**C**ACGCGCAC	2814
	GTGCGCGT**G**CAGGTCGC	2815
Haemoglobin variant Lys90Asn AAGc-AAC	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAA**G**CTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG	2816

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAG**C**TTGTGCGCGTGCAGGTCGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2817
	GCGCACAA**G**CTTCGGGT	2818
	ACCCGAAG**C**TTGTGCGC	2819
Haemoglobin variant Lys90Thr AAG-ACG	TGGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTG AGCGACCTGCACGCGCACA**A**GCTTCGGGTGGACCCGGTCAA CTTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGA	2820
	TCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGTT GACCGGGTCCACCCGAAGC**T**TGTGCGCGTGCAGGTCGCTCA GGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCCA	2821
	CGCGCACA**A**GCTTCGGG	2822
	CCCGAAGC**T**TGTGCGCG	2823
Haemoglobin variant Arg92Gln CGG-CAG	ACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGAC CTGCACGCGCACAAGCTTC**G**GGTGGACCCGGTCAACTTCAA GGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAGGGGCG	2824
	CGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTT GAAGTTGACCGGGTCCACC**C**GAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGT	2825
	CAAGCTTC**G**GGTGGACC	2826
	GGTCCACC**C**GAAGCTTG	2827
Haemoglobin variant Asp94Gly GAC-GGC	ACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCAC GCGCACAAGCTTCGGGTGG**A**CCCGGTCAACTTCAAGGTGAG CGGCGGGCCGGGAGCGATCTGGGTCGAGGGGCGAGATGG	2828
	CCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCT CACCTTGAAGTTGACCGGG**T**CCACCCGAAGCTTGTGCGCGT GCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGT	2829
	TCGGGTGG**A**CCCGGTCA	2830
	TGACCGGG**T**CCACCCGA	2831
Haemoglobin variant Pro95Arg CCG-CGG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACC**C**GGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTCGAGGGGCGAGATGGCGC	2832
	GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACC**G**GGTCCACCCGAAGCTTGTGCG CGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT	2833
	GGTGGACC**C**GGTCAACT	2834
	AGTTGACC**G**GGTCCACC	2835
Haemoglobin variant Ser102Arg AGCc-AGA	CGGCGGCTGCGGGCCTGGGCCCTCGGCCCCACTGACCCTC TTCTCTGCACAGCTCCTAAG**C**CACTGCCTGCTGGTGACCCTG GCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC	2836
	GTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCC AGGGTCACCAGCAGGCAGTG**G**CTTAGGAGCTGTGCAGAGAA GAGGGTCAGTGGGGCCGAGGGCCCAGGCCCGCAGCCGCCG	2837
	CTCCTAAG**C**CACTGCCT	2838

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCAGTGGCTTAGGAG	2839
Haemoglobin variant Glu116Lys cGAG-AAG	TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGC CTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGC	2840
	GCACGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCG TGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCA GGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA	2841
	TCCCCGCCGAGTTCACC	2842
	GGTGAACTCGGCGGGGA	2843
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCCTGGCTTCTGTGAGCACCGTGCTGACCTCCAAATA	2844
	TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAACTTG TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	2845
	CACCCCTGCGGTGCACG	2846
	CGTGCACCGCAGGGGTG	2847
Thalassaemia alpha Leu129Pro CTG-CCG	TGGCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC GCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCTG ACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCAT	2848
	ATGGCCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC ACGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTG CACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCA	2849
	CAAGTTCCTGGCTTCTG	2850
	CAGAAGCCAGGAACTTG	2851
Haemoglobin variant Arg141Leu CGT-CTT	TGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCG TGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTGGCCA TGCTTCTTGCCCCTTGGGCCTCCCCCCAGCCCCTCCT	2852
	AGGAGGGGCTGGGGGGAGGCCCAAGGGGCAAGAAGCATGG CCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACG GTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTGCA	2853
	CAAATACCGTTAAGCTG	2854
	CAGCTTAACGGTATTTG	2855

EXAMPLE 16

Alpha-thalassemia - Hemoglobin alpha locus 2

The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 2 oligonucleotides of the invention.

Table 23
HBA2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Met(-1)Thr ATG-ACG	CCTGGCGCGCTCGCGGGCCGGCACTCTTCTGGTCCCCACAG ACTCAGAGAGAACCCACCA**T**GGTGCTGTCTCCTGCCGACAAG ACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCA	2856
	TGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTT GTCGGCAGGAGACAGCACC**A**TGGTGGGTTCTCTCTGAGTCT GTGGGGACCAGAAGAGTGCCGGCCCGCGAGCGCGCCAGG	2857
	ACCCACCA**T**GGTGCTGT	2858
	ACAGCACC**A**TGGTGGGT	2859
Haemoglobin variant Ala12Asp GCC-GAC	CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCC GACAAGACCAACGTCAAGG**C**CGCCTGGGGTAAGGTCGGCGC GCACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG	2860
	CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCCAGGCG**G**CCTTGACGTTGGTCTTGTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG	2861
	CGTCAAGG**C**CGCCTGGG	2862
	CCCAGGCG**G**CCTTGACG	2863
Haemoglobin variant Lys16Glu tAAG-GAG	AGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCAAC GTCAAGGCCGCCTGGGGT**A**AGGTCGGCGCGCACGCTGGCG AGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC	2864
	GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCT**T**ACCCCAGGCGGCCTTGACGTT GGTCTTGTCGGCAGGAGACAGCACCATGGTGGGTTCTCT	2865
	CCTGGGGT**A**AGGTCGGC	2866
	GCCGACCT**T**ACCCCAGG	2867
Haemoglobin variant His20Gln CACg-CAA	GGTGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCT GGGGTAAGGTCGGCGCGCA**C**GCTGGCGAGTATGGTGCGGA GGCCCTGGAGAGGTGAGGCTCCCTCCCCTGCTCCGACCCG	2868
	CGGGTCGGAGCAGGGGAGGGAGCCTCACCTCTCCAGGGCC TCCGCACCATACTCGCCAGC**G**TGCGCGCCGACCTTACCCCA GGCGGCCTTGACGTTGGTCTTGTCGGCAGGAGACAGCACC	2869
	GGCGCGCA**C**GCTGGCGA	2870
	TCGCCAGC**G**TGCGCGCC	2871
Haemoglobin variant Glu27Asp GAGg-GAC	GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGA**G**GCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGAC C	2872
	GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGC**C**TCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTC	2873
	GGTGCGGA**G**GCCCTGGA	2874
	TCCAGGGC**C**TCCGCACC	2875

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Thalassaemia alpha Leu29Pro CTG-CCG	ACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCC**T**GGAGAGGTGAGGCTCCCTCC CCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGACCCACAG	2876
	CTGTGGGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGG GGAGGGAGCCTCACCTCTCC**A**GGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCCAGGCGGCCTTGACGT	2877
	GGAGGCCC**T**GGAGAGGT	2878
	ACCTCTCC**A**GGGCCTCC	2879
Haemoglobin variant Asp47His cGAC-CAC	GCTTCTCCCCGCAGGATGTTCCTGTCCTTCCCCACCACCAAG ACCTACTTCCCGCACTTC**G**ACCTGAGCCACGGCTCTGCCCA GGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGA	2880
	TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTGG GCAGAGCCGTGGCTCAGGT**C**GAAGTGCGGGAAGTAGGTCTT GGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAGAAGC	2881
	CGCACTTC**G**ACCTGAGC	2882
	GCTCAGGT**C**GAAGTGCG	2883
Haemoglobin variant Leu48Arg CTG-CGG	CTCCCCGCAGGATGTTCCTGTCCTTCCCCACCACCAAGACCT ACTTCCCGCACTTCGACC**T**GAGCCACGGCTCTGCCCAGGTTA AGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACCAA	2884
	TTGGTCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAAC CTGGGCAGAGCCGTGGCTC**A**GGTCGAAGTGCGGGAAGTAG GTCTTGGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAG	2885
	CTTCGACC**T**GAGCCACG	2886
	CGTGGCTC**A**GGTCGAAG	2887
Haemoglobin variant Gln54Glu cCAG-GAG	CTGTCCTTCCCCACCACCAAGACCTACTTCCCGCACTTCGAC CTGAGCCACGGCTCTGCC**C**AGGTTAAGGGCCACGGCAAGAA GGTGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGG	2888
	CCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACCTTC TTGCCGTGGCCCTTAACCT**G**GGCAGAGCCGTGGCTCAGGTC GAAGTGCGGGAAGTAGGTCTTGGTGGTGGGGAAGGACAG	2889
	GCTCTGCC**C**AGGTTAAG	2890
	CTTAACCT**G**GGCAGAGC	2891
Haemoglobin variant Gly59Asp GGC-GAC	CCAAGACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTG CCCAGGTTAAGGGCCACG**G**CAAGAAGGTGGCCGACGCGCT GACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGC	2892
	GCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAG CGCGTCGGCCACCTTCTTG**C**CGTGGCCCTTAACCTGGGCAG AGCCGTGGCTCAGGTCGAAGTGCGGGAAGTAGGTCTTGG	2893
	GGGCCACG**G**CAAGAAGG	2894
	CCTTCTTG**C**CGTGGCCC	2895
Haemoglobin variant Asn68Lys AACg-AAG	GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA**C**GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2896

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGC**G**TTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2897
	CTGACCAA**C**GCCGTGGC	2898
	GCCACGGC**G**TTGGTCAG	2899
Haemoglobin variant Asn68Lys AACg-AAA	GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA**C**GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG	2900
	CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATG TCGTCCACGTGCGCCACGGC**G**TTGGTCAGCGCGTCGGCCAC CTTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC	2901
	CTGACCAA**C**GCCGTGGC	2902
	GCCACGGC**G**TTGGTCAG	2903
Haemoglobin variant Asn78Lys AACg-AAA	CGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGGCG CACGTGGACGACATGCCCAA**C**GCGCTGTCCGCCCTGAGCGA CCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTTC	2904
	GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGC**G**TTGGGCATGTCGTCCACGTGC GCCACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCG	2905
	ATGCCCAA**C**GCGCTGTC	2906
	GACAGCGC**G**TTGGGCAT	2907
Haemoglobin variant Asp85Val GAC-GTC	CGCTGACCAACGCCGTGGCGCACGTGGACGACATGCCCAAC GCGCTGTCCGCCCTGAGCG**A**CCTGCACGCGCACAAGCTTCG GGTGGACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGG	2908
	CCCGGCCCGCCGCTCACCTTGAAGTTGACCGGGTCCACCCG AAGCTTGTGCGCGTGCAGG**T**CGCTCAGGGCGGACAGCGCGT TGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAGCG	2909
	CCTGAGCG**A**CCTGCACG	2910
	CGTGCAGG**T**CGCTCAGG	2911
Haemoglobin variant Lys90Asn AAGc-AAT	GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAA**G**CTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG	2912
	CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAG**C**TTGTGCGCGTGCAGGTCGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC	2913
	GCGCACAA**G**CTTCGGGT	2914
	ACCCGAAG**C**TTGTGCGC	2915
Haemoglobin variant Asp94His gGAC-CAC	GACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCA CGCGCACAAGCTTCGGGTG**G**ACCCGGTCAACTTCAAGGTGA GCGGCGGGCCGGGAGCGATCTGGGTCGAGGGGCGAGATG	2916
	CATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTC ACCTTGAAGTTGACCGGGT**C**CACCCGAAGCTTGTGCGCGTG CAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTC	2917
	TTCGGGTG**G**ACCCGGTC	2918

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GACCGGGTCCACCCGAA	2919
Haemoglobin variant Pro95Leu CCG-CTG	ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTCGAGGGGCGAGATGGCGC	2920
	GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT	2921
	GGTGGACCCGGTCAACT	2922
	AGTTGACCGGGTCCACC	2923
Haemoglobin variant Ser102Arg aAGC-CGC	TAGCGCAGGCGGCGGCTGCGGGCCTGGGCCGCACTGACCC TCTTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCC TGGCCGCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGC	2924
	GCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGCCAG GGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAAGA GGGTCAGTGCGGCCCAGGCCCGCAGCCGCCGCCTGCGCTA	2925
	AGCTCCTAAGCCACTGC	2926
	GCAGTGGCTTAGGAGCT	2927
Haemoglobin H disease Cys104Tyr TGC-TAC	GGCGGCGGCTGCGGGCCTGGGCCGCACTGACCCTCTTCTCT GCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGC CCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC	2928
	GAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGG CGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCA GAGAAGAGGGTCAGTGCGGCCCAGGCCCGCAGCCGCCGCC	2929
	AAGCCACTGCCTGCTGG	2930
	CCAGCAGGCAGTGGCTT	2931
Haemoglobin variant Ala111Val GCC-GTC	CCGCACTGACCCTCTTCTCTGCACAGCTCCTAAGCCACTGCC TGCTGGTGACCCTGGCCGCCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTC	2932
	GAAGCCAGGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGG CAGTGGCTTAGGAGCTGTGCAGAGAAGAGGGTCAGTGCGG	2933
	CCTGGCCGCCCACCTCC	2934
	GGAGGTGGGCGGCCAGG	2935
Haemoglobin variant Ala120Glu GCG-GAG	TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCCTGGCTTCTGTGAGCACCGTGCTGACCTCCAAATA	2936
	TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAACTTG TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA	2937
	CACCCCTGCGGTGCACG	2938
	CGTGCACCGCAGGGGTG	2939
Haemoglobin variant His122Gln CACg-CAG	CCACTGCCTGCTGGTGACCCTGGCCGCCCACCTCCCCGCCG AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAA	2940

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGC**G**TGCACCGCAGGGGTGAACTCGG CGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGG	2941
	GCGGTGCA**C**GCCTCCCT	2942
	AGGGAGGC**G**TGCACCGC	2943
Haemoglobin variant Ala123Ser cGCC-TCC	CACTGCCTGCTGGTGACCCTGGCCGCCCACCTCCCCGCCGA GTTCACCCCTGCGGTGCAC**G**CCTCCCTGGACAAGTTCCTGG CTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAG	2944
	CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGAACTTGTCCAGGGAGG**C**GTGCACCGCAGGGGTGAACTCG GCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTG	2945
	CGGTGCAC**G**CCTCCCTG	2946
	CAGGGAGG**C**GTGCACCG	2947
Thalassaemia alpha Leu125Pro CTG-CCG	TGCTGGTGACCCTGGCCGCCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCC**T**GGACAAGTTCCTGGCTTCTGT GAGCACCGTGCTGACCTCCAAATACCGTTAAGCTGGAGC	2948
	GCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGTGCTCACA GAAGCCAGGAACTTGTCC**A**GGGAGGCGTGCACCGCAGGGG TGAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCA	2949
	CGCCTCCC**T**GGACAAGT	2950
	ACTTGTCC**A**GGGAGGCG	2951
Haemoglobin variant Ser131Pro tTCT-CCT	GCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC CCTGGACAAGTTCCTGGCT**T**CTGTGAGCACCGTGCTGACCTC CAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCCTC	2952
	GAGGAACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAG GTCAGCACGGTGCTCACAG**A**AGCCAGGAACTTGTCCAGGGA GGCGTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGC	2953
	TCCTGGCT**T**CTGTGAGC	2954
	GCTCACAG**A**AGCCAGGA	2955
Haemoglobin variant Leu136Met gCTG-ATG	GAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCT GGCTTCTGTGAGCACCGTG**C**TGACCTCCAAATACCGTTAAGC TGGAGCCTCGGTAGCCGTTCCTCCTGCCCGCTGGGCCT	2956
	AGGCCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAGC TTAACGGTATTTGGAGGTCA**G**CACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTC	2957
	GCACCGTG**C**TGACCTCC	2958
	GGAGGTCA**G**CACGGTGC	2959
Haemoglobin variant Leu136Pro CTG-CCG	AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGC**T**GACCTCCAAATACCGTTAAGCT GGAGCCTCGGTAGCCGTTCCTCCTGCCCGCTGGGCCTC	2960
	GAGGCCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAG CTTAACGGTATTTGGAGGTC**A**GCACGGTGCTCACAGAAGCCA GGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACT	2961
	CACCGTGC**T**GACCTCCA	2962

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGGAGGTCAGCACGGTG	2963
Haemoglobin variant Arg141Cys cCGT-TGT	GTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACC GTGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCC GTTCCTCCTGCCCGCTGGGCCTCCCAACGGGCCCTCC	2964
	GGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAACGGC TACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGT GCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTGCAC	2965
	CCAAATACCGTTAAGCT	2966
	AGCTTAACGGTATTTGG	2967
Haemoglobin variant Term142Gln tTAA-CAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGCCCTCCTCC	2968
	GGAGGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTG	2969
	AATACCGTTAAGCTGGA	2970
	TCCAGCTTAACGGTATT	2971
Haemoglobin variant Term142Lys tTAA-AAA	CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGCCCTCCTCC	2972
	GGAGGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTG	2973
	AATACCGTTAAGCTGGA	2974
	TCCAGCTTAACGGTATT	2975
Haemoglobin variant Term142Tyr TAAg-TAT	CGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCT GACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCC TCCTGCCCGCTGGGCCTCCCAACGGGCCCTCCTCCCC	2976
	GGGGAGGAGGGCCCGTTGGGAGGCCCAGCGGGCAGGAGG AACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAG CACGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCG	2977
	TACCGTTAAGCTGGAGC	2978
	GCTCCAGCTTAACGGTA	2979

EXAMPLE 17
Human mismatch repair - MLH1

The human MLH1 gene is homologous to the bacterial *mutL* gene, which is involved in mismatch repair. Mutations in the MLH1 gene have been identified in many individuals with hereditary nonpolyposis colorectal cancer (HNPCC). Mutations in the MLH1 gene are also implicated in predisposition to a variety of cancers associated with, for example, Muir-Torre syndrome and Turcot

syndrome. The attached table discloses the correcting oligonucleotide base sequences for the MLH1 oligonucleotides of the invention.

Table 24
MLH1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Met1Arg ATG-AGG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2980
	GCCGCGATGCGGTTCACCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2981
	CGCCAAAATGTCGTTCG	2982
	CGAACGACATTTTGGCG	2983
Non-polyposis colorectal cancer Met1Lys ATG-AAG	TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC	2984
	GCCGCGATGCGGTTCACCACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA	2985
	CGCCAAAATGTCGTTCG	2986
	CGAACGACATTTTGGCG	2987
Non-polyposis colorectal cancer Met35Arg ATG-AGG	TGGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCA GCTAATGCTATCAAAGAGATGATTGAGAACTGGTACGGAGGG AGTCGAGCCGGGCTCACTTAAGGGCTACGACTTAACGG	2988
	CCGTTAAGTCGTAGCCCTTAAGTGAGCCCGGCTCGACTCCCT CCGTACCAGTTCTCAATCATCTCTTTGATAGCATTAGCTGGCC GCTGGATAACTTCCCCCGCCGCGATGCGGTTCACCA	2989
	CAAAGAGATGATTGAGA	2990
	TCTCAATCATCTCTTTG	2991
Non-polyposis colorectal cancer Ser44Phe TCC-TTC	TAGAGTAGTTGCAGACTGATAAATTATTTTCTGTTTGATTTGCC AGTTTAGATGCAAAATCCACAAGTATTCAAGTGATTGTTAAAG AGGGAGGCCTGAAGTTGATTCAGATCCAAGACAA	2992
	TTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAA TCACTTGAATACTTGTGGATTTTGCATCTAAACTGGCAAATCA AACAGAAAATAATTTATCAGTCTGCAACTACTCTA	2993
	TGCAAAATCCACAAGTA	2994
	TACTTGTGGATTTTGCA	2995
Non-polyposis colorectal cancer Gln62Lys CAA-AAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGG GTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGC	2996

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	2997
	TTCAGATCCAAGACAAT	2998
	ATTGTCTTGGATCTGAA	2999
Non-polyposis colorectal cancer Gln62Term CAA-TAA	GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGGGTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGC	3000
	GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAATACTTGTGGATTTTGC	3001
	TTCAGATCCAAGACAAT	3002
	ATTGTCTTGGATCTGAA	3003
Non-polyposis colorectal cancer Asn64Ser AAT-AGT	CCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGGGTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGG	3004
	CCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAATACTTGTGG	3005
	CCAAGACAATGGCACCG	3006
	CGGTGCCATTGTCTTGG	3007
Non-polyposis colorectal cancer Gly67Arg GGG-AGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGGGTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3008
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3009
	ATGGCACCGGGATCAGG	3010
	CCTGATCCCGGTGCCAT	3011
Non-polyposis colorectal cancer Gly67Arg GGG-CGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGGGTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3012
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3013
	ATGGCACCGGGATCAGG	3014
	CCTGATCCCGGTGCCAT	3015
Non-polyposis colorectal cancer Gly67Trp GGG-TGG	ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTCAGATCCAAGACAATGGCACCGGGATCAGGGTAAGTAAAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA	3016
	TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGATCCCGGTGCCATTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT	3017
	ATGGCACCGGGATCAGG	3018

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCTGATCCCGGTGCCAT	3019
Non-polyposis colorectal cancer Cys77Arg TGT-CGT	GTAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGA AGATCTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTG CAGTCCTTTGAGGATTTAGCCAGTATTTCTACCT	3020
	AGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTACT AGTAGTGAACCTTTCACATACAATATCCAGATCTTCTTTCTGTT AGATACCAAAAAGATGAGTAAATAATCATGTTAC	3021
	ATATTGTATGTGAAAGG	3022
	CCTTTCACATACAATAT	3023
Non-polyposis colorectal cancer Cys77Tyr TGT-TAT	TAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGAA GATCTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTGC AGTCCTTTGAGGATTTAGCCAGTATTTCTACCTA	3024
	TAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTAC TAGTAGTGAACCTTTCACCATACAATATCCAGATCTTCTTTCTGT TAGATACCAAAAAGATGAGTAAATAATCATGTTA	3025
	TATTGTATGTGAAAGGT	3026
	ACCTTTCACCATACAATA	3027
Non-polyposis colorectal cancer Ser93Gly AGT-GGT	CTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTGCAGT CCTTTGAGGATTTAGCCAGTATTTCTACCTATGGCTTTCGAGG TGAGGTAAGCTAAAGATTCAAGAAATGTGTAAAAT	3028
	ATTTTACACATTTCTTGAATCTTTAGCTTACCTCACCTCGAAAG CCATAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTT TACTAGTAGTGAACCTTTCACATACAATATCCAG	3029
	ATTTAGCCAGTATTTCT	3030
	AGAAATACTGGCTAAAT	3031
Non-polyposis colorectal cancer Arg100Term CGA-TGA	TTCACTACTAGTAAACTGCAGTCCTTTGAGGATTTAGCCAGTA TTTCTACCTATGGCTTTCGAGGTGAGGTAAGCTAAAGATTCAA GAAATGTGTAAAATATCCTCCTGTGATGACATTGT	3032
	ACAATGTCATCACAGGAGGATATTTTACACATTTCTTGAATCTT TAGCTTACCTCACCTCGAAAGCCATAGGTAGAAATACTGGCTA AATCCTCAAAGGACTGCAGTTTACTAGTAGTGAA	3033
	ATGGCTTTCGAGGTGAG	3034
	CTCACCTCGAAAGCCAT	3035
Non-polyposis colorectal cancer Ile107Arg ATA-AGA	ACCCAGCAGTGAGTTTTTCTTTCAGTCTATTTTCTTTTCTTCCT TAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTA CAACGAAAACAGCTGATGGAAAGTGTGCATACAG	3036
	CTGTATGCACACTTTCCATCAGCTGTTTTCGTTGTAATAGTAA CATGAGCCACATGGCTTATGCTGGCCAAAGCCTAAGGAAGAA AAGAAAATAGACTGAAAGAAAAACTCACTGCTGGGT	3037
	GGCCAGCATAAGCCATG	3038
	CATGGCTTATGCTGGCC	3039

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Thr117Arg ACG-AGG	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCATACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3040
	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACTTTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATGGCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3041
	TATTACAACGAAAACAG	3042
	CTGTTTTCGTTGTAATA	3043
Non-polyposis colorectal cancer Thr117Met ACG-ATG	TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCATACAGGTATAGTGCTGACTTCTTTTACTCATATAT	3044
	ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACTTTCCATCAGCTGTTTTCGTTGTAATAGTAACATGAGCCACATGGCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA	3045
	TATTACAACGAAAACAG	3046
	CTGTTTTCGTTGTAATA	3047
Non-polyposis colorectal cancer Gly133Term GGA-TGA	TCTATCTCTCTACTGGATATTAATTTGTTATATTTTCTCATTAGAGCAAGTTACTCAGATGGAAAACTGAAAGCCCCTCCTAAACCATGTGCTGGCAATCAAGGGACCCAGATCACGGTAA	3048
	TTACCGTGATCTGGGTCCCTTGATTGCCAGCACATGGTTTAGGAGGGGCTTTCAGTTTTCCATCTGAGTAACTTGCTCTAATGAGAAAATATAACAAATTAATATCCAGTAGAGAGATAGA	3049
	ACTCAGATGGAAAACTG	3050
	CAGTTTTCCATCTGAGT	3051
Non-polyposis colorectal cancer Val185Gly GTA-GGA	TAGTGTGTGTTTTTGGCAACTCTTTTCTTACTCTTTTGTTTTTCTTTTCCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAGTTAAAAAAGTAAGTTCTTGGTTTATGGGGGATGG	3052
	CCATCCCCCATAAACCAAGAACTTACTTTTTTAACTGAGAAACTAATGCCTGCATTGTGTACTGAATACCTGGAAAAGAAAAACAAAAGAGTAAGAAAAGAGTTGCCAAAAACACACACTA	3053
	GTATTCAGTACACAATG	3054
	CATTGTGTACTGAATAC	3055
Non-polyposis colorectal cancer Ser193Pro TCA-CCA	TTTCTTACTCTTTTGTTTTTCTTTTCCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAGTTAAAAAAGTAAGTTCTTGGTTTATGGGGGATGGTTTTGTTTTATGAAAAGAAAAAA	3056
	TTTTTTCTTTTCATAAAACAAAACCATCCCCCATAAACCAAGAACTTACTTTTTTAACTGAGAAACTAATGCCTGCATTGTGTACTGAATACCTGGAAAAGAAAAACAAAAGAGTAAGAAA	3057
	TTAGTTTCTCAGTTAAA	3058
	TTTAACTGAGAAACTAA	3059
Non-polyposis colorectal cancer Val213Met GTG-ATG	TTTGTTTATCAGCAAGGAGAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACCGTGGACAATATTCGCTCCATCTTTGGAAATGCTGTTAGTCGGTATGTCGATAACCTATATA	3060

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGATGGAGCGAATATTGTCCA**C**GGTTGAGGCATTGGGTAGTGTCCTAACATCAGCTACTGTCTCTCCTTGCTGATAAACAAA	3061
	CCTCAACC**G**TGGACAAT	3062
	ATTGTCCA**C**GGTTGAGG	3063
Non-polyposis colorectal cancer Arg217Cys CGC-TGC	CAAGGAGAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACCGTGGACAATATT**C**GCTCCATCTTTGGAAATGCTGTTAGTCGGTATGTCGATAACCTATATAAAAAAATCTTTT	3064
	AAAAGATTTTTTTATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGATGGAGC**G**AATATTGTCCACGGTTGAGGCATTGGGTAGTGTCCTAACATCAGCTACTGTCTCTCCTTG	3065
	ACAATATT**C**GCTCCATC	3066
	GATGGAGC**G**AATATTGT	3067
Non-polyposis colorectal cancer Ile219Val ATC-GTC	GAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACCGTGGACAATATTCGCTCC**A**TCTTTGGAAATGCTGTTAGTCGGTATGTCGATAACCTATATAAAAAAATCTTTTACATTT	3068
	AAATGTAAAAGATTTTTTTATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGA**T**GGAGCGAATATTGTCCACGGTTGAGGCATTGGGTAGTGTCCTAACATCAGCTACTGTCTC	3069
	TTCGCTCC**A**TCTTTGGA	3070
	TCCAAAGA**T**GGAGCGAA	3071
Non-polyposis colorectal cancer Gly244Asp GGT-GAT	CTAATAGAGAACTGATAGAAATTGGATGTGAGGATAAAACCCTAGCCTTCAAAATGAATG**G**TTACATATCCAATGCAAACTACTCAGTGAAGAAGTGCATCTTCTTACTCTTCATCAACCG	3072
	CGGTTGATGAAGAGTAAGAAGATGCACTTCTTCACTGAGTAGTTTGCATTGGATATGTAA**C**CATTCATTTTGAAGGCTAGGGTTTTATCCTCACATCCAATTTCTATCAGTTCTCTATTAG	3073
	AATGAATG**G**TTACATAT	3074
	ATATGTAA**C**CATTCATT	3075
Non-polyposis colorectal cancer Ser252Term TCA-TAA	GATGTGAGGATAAAACCCTAGCCTTCAAAATGAATGGTTACATATCCAATGCAAACTACT**C**AGTGAAGAAGTGCATCTTCTTACTCTTCATCAACCGTAAGTTAAAAAGAACCACATGGGA	3076
	TCCCATGTGGTTCTTTTTAACTTACGGTTGATGAAGAGTAAGAAGATGCACTTCTTCACT**G**AGTAGTTTGCATTGGATATGTAACCATTCATTTTGAAGGCTAGGGTTTTATCCTCACATC	3077
	AAACTACT**C**AGTGAAGA	3078
	TCTTCACT**G**AGTAGTTT	3079
Non-polyposis colorectal cancer Glu268Gly GAA-GGA	CACCCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTTATTGTTTAGATCGTCTGGTAG**A**ATCAACTTCCTTGAGAAAAGCCATAGAAACAGTGTATGCAGCCTATTTGCCCAAAAACAC	3080
	GTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGGCTTTTCTCAAGGAAGTTGAT**T**CTACCAGACGATCTAAACAATAAAAAGAAAGCAACCAGTTCAAAACTGTCCTGAGGGGTG	3081
	TCTGGTAG**A**ATCAACTT	3082

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AAGTTGATTCTACCAGA	3083
Non-polyposis colorectal cancer Ser269Term TCA-TGA	CCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTTATTGTTTA GATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATAGAAA CAGTGTATGCAGCCTATTTGCCCAAAAACACACA	3084
	TGTGTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGG CTTTTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATA AAAAGAAAGCAACCAGTTCAAAACTGTCCTGAGGG	3085
	GGTAGAATCAACTTCCT	3086
	AGGAAGTTGATTCTACC	3087
Non-polyposis colorectal cancer Glu297Term GAA-TAA	CTTTTTCTCCCCCTCCCACTATCTAAGGTAATTGTTCTCTCTTA TTTTCCTGACAGTTTAGAAATCAGTCCCCAGAATGTGGATGTT AATGTGCACCCCACAAAGCATGAAGTTCACTTCC	3088
	GGAAGTGAACTTCATGCTTTGTGGGGTGCACATTAACATCCA CATTCTGGGGACTGATTTCTAAACTGTCAGGAAAATAAGAGAG AACAATTACCTTAGATAGTGGGAGGGGGAGAAAAAG	3089
	ACAGTTTAGAAATCAGT	3090
	ACTGATTTCTAAACTGT	3091
Non-polyposis colorectal cancer Gln301Term CAG-TAG	CTCCCACTATCTAAGGTAATTGTTCTCTCTTATTTTCCTGACAG TTTAGAAATCAGTCCCCAGAATGTGGATGTTAATGTGCACCCC ACAAAGCATGAAGTTCACTTCCTGCACGAGGAGA	3092
	TCTCCTCGTGCAGGAAGTGAACTTCATGCTTTGTGGGGTGCA CATTAACATCCACATTCTGGGGACTGATTTCTAAACTGTCAGG AAAATAAGAGAGAACAATTACCTTAGATAGTGGGAG	3093
	TCAGTCCCCAGAATGTG	3094
	CACATTCTGGGGACTGA	3095
Non-polyposis colorectal cancer Val326Ala GTG-GCG	ATGTGCACCCCACAAAGCATGAAGTTCACTTCCTGCACGAGG AGAGCATCCTGGAGCGGGTGCAGCAGCACATCGAGAGCAAG CTCCTGGGCTCCAATTCCTCCAGGATGTACTTCACCCA	3096
	TGGGTGAAGTACATCCTGGAGGAATTGGAGCCCAGGAGCTT GCTCTCGATGTGCTGCTGCACCCGCTCCAGGATGCTCTCCT CGTGCAGGAAGTGAACTTCATGCTTTGTGGGGTGCACAT	3097
	GGAGCGGGTGCAGCAGC	3098
	GCTGCTGCACCCGCTCC	3099
Non-polyposis colorectal cancer His329Pro CAC-CCC	CCACAAAGCATGAAGTTCACTTCCTGCACGAGGAGAGCATCC TGGAGCGGGTGCAGCAGCACATCGAGAGCAAGCTCCTGGGC TCCAATTCCTCCAGGATGTACTTCACCCAGGTCAGGGC	3100
	GCCCTGACCTGGGTGAAGTACATCCTGGAGGAATTGGAGCC CAGGAGCTTGCTCTCGATGTGCTGCTGCACCCGCTCCAGGA TGCTCTCCTCGTGCAGGAAGTGAACTTCATGCTTTGTGG	3101
	GCAGCAGCACATCGAGA	3102
	TCTCGATGTGCTGCTGC	3103

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Val384Asp GTT-GAT	CAAGTCTGACCTCGTCTTCTACTTCTGGAAGTAGTGATAAGGT CTATGCCCACCAGATGG**T**TCGTACAGATTCCCGGGAACAGAA GCTTGATGCATTTCTGCAGCCTCTGAGCAAACCCCT	3104
	AGGGGTTTGCTCAGAGGCTGCAGAAATGCATCAAGCTTCTGT TCCCGGGAATCTGTACGA**A**CCATCTGGTGGGCATAGACCTTA TCACTACTTCCAGAAGTAGAAGACGAGGTCAGACTTG	3105
	CCAGATGG**T**TCGTACAG	3106
	CTGTACGA**A**CCATCTGG	3107
Non-polyposis colorectal cancer Ala441Thr GCT-ACT	AGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAACT CCCAGCCCCTGCTGAAGTG**G**CTGCCAAAAATCAGAGCTTGGA GGGGGATACAACAAAGGGGACTTCAGAAATGTCAGAGA	3108
	TCTCTGACATTTCTGAAGTCCCCTTTGTTGTATCCCCCTCCAA GCTCTGATTTTTGGCAG**C**CACTTCAGCAGGGGCTGGGAGTTC AAGCATCTCCTCATCTTGCTGCCTAGCCCTGCCACT	3109
	CTGAAGTG**G**CTGCCAAA	3110
	TTTGGCAG**C**CACTTCAG	3111
Non-polyposis colorectal cancer Arg487Term CGA-TGA	CTTCATTGCAGAAAGAGACATCGGGAAGATTCTGATGTGGAA ATGGTGGAAGATGATTCC**C**GAAAGGAAATGACTGCAGCTTGT ACCCCCCGGAGAAGGATCATTAACCTCACTAGTGTTT	3112
	AAACACTAGTGAGGTTAATGATCCTTCTCCGGGGGGTACAAG CTGCAGTCATTTCCTTTC**G**GGAATCATCTTCCACCATTTCCAC ATCAGAATCTTCCCGATGTCTCTTTCTGCAATGAAG	3113
	ATGATTCC**C**GAAAGGAA	3114
	TTCCTTTC**G**GGAATCAT	3115
Non-polyposis colorectal cancer Ala492Thr GCA-ACA	AGACATCGGGAAGATTCTGATGTGGAAATGGTGGAAGATGAT TCCCGAAAGGAAATGACT**G**CAGCTTGTACCCCCCGGAGAAG GATCATTAACCTCACTAGTGTTTTGAGTCTCCAGGAAG	3116
	CTTCCTGGAGACTCAAAACACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTG**C**AGTCATTTCCTTTCGGGAATCATC TTCCACCATTTCCACATCAGAATCTTCCCGATGTCT	3117
	AAATGACT**G**CAGCTTGT	3118
	ACAAGCTG**C**AGTCATTT	3119
Non-polyposis colorectal cancer Val506Ala GTT-GCT	CCCGAAAGGAAATGACTGCAGCTTGTACCCCCCGGAGAAGG ATCATTAACCTCACTAGTG**T**TTTGAGTCTCCAGGAAGAAATTA ATGAGCAGGGACATGAGGGTACGTAAACGCTGTGGCC	3120
	GGCCACAGCGTTTACGTACCCTCATGTCCCTGCTCATTAATTT CTTCCTGGAGACTCAAA**A**CACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTGCAGTCATTTCCTTTCGGG	3121
	CACTAGTG**T**TTTGAGTC	3122
	GACTCAAA**A**CACTAGTG	3123
Non-polyposis colorectal cancer Gln542Leu CAG-CTG	GGGAGATGTTGCATAACCACTCCTTCGTGGGCTGTGTGAATC CTCAGTGGGCCTTGGCAC**A**GCATCAAACCAAGTTATACCTTC TCAACACCACCAAGCTTAGGTAAATCAGCTGAGTGTG	3124

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACACTCAGCTGATTTACCTAAGCTTGGTGGTGTTGAGAAGG TATAACTTGGTTTGATGCTGTGCCAAGGCCCACTGAGGATTC ACACAGCCCACGAAGGAGTGGTTATGCAACATCTCCC	3125
	CTTGGCACAGCATCAAA	3126
	TTTGATGCTGTGCCAAG	3127
Non-polyposis colorectal cancer Leu549Pro CTT-CCT	CCTTCGTGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAG CATCAAACCAAGTTATACCTTCTCAACACCACCAAGCTTAGGT AAATCAGCTGAGTGTGTGAACAAGCAGAGCTACTACA	3128
	TGTAGTAGCTCTGCTTGTTCACACACTCAGCTGATTTACCTAA GCTTGGTGGTGTTGAGAAGGTATAACTTGGTTTGATGCTGTG CCAAGGCCCACTGAGGATTCACACAGCCCACGAAGG	3129
	GTTATACCTTCTCAACA	3130
	TGTTGAGAAGGTATAAC	3131
Non-polyposis colorectal cancer Asn551Thr AAC-ACC	TGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAGCATCAAA CCAAGTTATACCTTCTCAACACCACCAAGCTTAGGTAAATCAG CTGAGTGTGTGAACAAGCAGAGCTACTACAACAATG	3132
	CATTGTTGTAGTAGCTCTGCTTGTTCACACACTCAGCTGATTT ACCTAAGCTTGGTGGTGTTGAGAAGGTATAACTTGGTTTGATG CTGTGCCAAGGCCCACTGAGGATTCACACAGCCCA	3133
	CCTTCTCAACACCACCA	3134
	TGGTGGTGTTGAGAAGG	3135
Non-polyposis colorectal cancer Gln562Term CAG-TAG	ATGAATTCAGCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAG TGAAGAACTGTTCTACCAGATACTCATTTATGATTTTGCCAATT TTGGTGTTCTCAGGTTATCGGTAAGTTTAGATC	3136
	GATCTAAACTTACCGATAACCTGAGAACACCAAAATTGGCAAA ATCATAAATGAGTATCTGGTAGAACAGTTCTTCACTGAAAATA AAAATGAAGTGACTTTAAGGAAAAGCTGAATTCAT	3137
	TGTTCTACCAGATACTC	3138
	GAGTATCTGGTAGAACA	3139
Non-polyposis colorectal cancer Ile565Phe ATT-TTT	GCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAGTGAAGAACT GTTCTACCAGATACTCATTTATGATTTTGCCAATTTTGGTGTTC TCAGGTTATCGGTAAGTTTAGATCCTTTTCACT	3140
	AGTGAAAAGGATCTAAACTTACCGATAACCTGAGAACACCAAA ATTGGCAAAATCATAAATGAGTATCTGGTAGAACAGTTCTTCA CTGAAAATAAAAATGAAGTGACTTTAAGGAAAAGC	3141
	AGATACTCATTTATGAT	3142
	ATCATAAATGAGTATCT	3143
Non-polyposis colorectal cancer Leu574Pro CTC-CCC	TTTTCAGTGAAGAACTGTTCTACCAGATACTCATTTATGATTTT GCCAATTTTGGTGTTCTCAGGTTATCGGTAAGTTTAGATCCTT TTCACTTCTGAAATTTCAACTGATCGTTTCTGAA	3144
	TTCAGAAACGATCAGTTGAAATTTCAGAAGTGAAAAGGATCTA AACTTACCGATAACCTGAGAACACCAAAATTGGCAAAATCATA AATGAGTATCTGGTAGAACAGTTCTTCACTGAAAA	3145
	TGGTGTTCTCAGGTTAT	3146

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAACCTGAGAACACCA	3147
Non-polyposis colorectal cancer Leu582Val CTC-GTC	TGGATGCTCCGTTAAAGCTTGCTCCTTCATGTTCTTGCTTCTT CCTAGGAGCCAGCACCGCTCTTTGACCTTGCCATGCTTGCCT TAGATAGTCCAGAGAGTGGCTGGACAGAGGAAGATG	3148
	CATCTTCCTCTGTCCAGCCACTCTCTGGACTATCTAAGGCAA GCATGGCAAGGTCAAAGAGCGGTGCTGGCTCCTAGGAAGAA GCAAGAACATGAAGGAGCAAGCTTTAACGGAGCATCCA	3149
	CAGCACCGCTCTTTGAC	3150
	GTCAAAGAGCGGTGCTG	3151
Non-polyposis colorectal cancer Leu607His CTT-CAT	TGCTTGCCTTAGATAGTCCAGAGAGTGGCTGGACAGAGGAAG ATGGTCCCAAAGAAGGACTTGCTGAATACATTGTTGAGTTTCT GAAGAAGAAGGCTGAGATGCTTGCAGACTATTTCTC	3152
	GAGAAATAGTCTGCAAGCATCTCAGCCTTCTTCTTCAGAAACT CAACAATGTATTCAGCAAGTCCTTCTTTGGGACCATCTTCCTC TGTCCAGCCACTCTCTGGACTATCTAAGGCAAGCA	3153
	AGAAGGACTTGCTGAAT	3154
	ATTCAGCAAGTCCTTCT	3155
Non-polyposis colorectal cancer Lys618Term AAG-TAG	ACAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATT GTTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTAT TTCTCTTTGGAAATTGATGAGGTGTGACAGCCATTCT	3156
	AGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGTC TGCAAGCATCTCAGCCTTCTTCTTCAGAAACTCAACAATGTAT TCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTGT	3157
	TGAAGAAGAAGGCTGAG	3158
	CTCAGCCTTCTTCTTCA	3159
Non-polyposis colorectal cancer Lys618Thr AAG-ACG	CAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATTG TTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTATTT CTCTTTGGAAATTGATGAGGTGTGACAGCCATTCTT	3160
	AAGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGT CTGCAAGCATCTCAGCCTTCTTCTTCAGAAACTCAACAATGTA TTCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTG	3161
	GAAGAAGAAGGCTGAGA	3162
	TCTCAGCCTTCTTCTTC	3163
Non-polyposis colorectal cancer Arg659Leu CGA-CTA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCGGTACATGCATGTGTGC	3164
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTCGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3165
	CATTCTTCGACTAGCCA	3166
	TGGCTAGTCGAAGAATG	3167

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Arg659Pro CGA-CCA	TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGACTGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCAAGCAGATACTAAGCATTTCGGTACATGCATGTGTGC	3168
	GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCACTGACCTCAGTGGCTAGTCGAAGAATGAAGATAGGCAGTCCCTCCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA	3169
	CATTCTTCGACTAGCCA	3170
	TGGCTAGTCGAAGAATG	3171
Non-polyposis colorectal cancer Arg659Term CGA-TGA	TTACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGACTGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCAAGCAGATACTAAGCATTTCGGTACATGCATGTGTG	3172
	CACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCACTGACCTCAGTGGCTAGTCGAAGAATGAAGATAGGCAGTCCCTCCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTAA	3173
	TCATTCTTCGACTAGCC	3174
	GGCTAGTCGAAGAATGA	3175
Non-polyposis colorectal cancer Ala681Thr GCT-ACT	TTGGACCAGGTGAATTGGGACGAAGAAAAGGAATGTTTTGAAAGCCTCAGTAAAGAATGCGCTATGTTCTATTCCATCCGGAAGCAGTACATATCTGAGGAGTCGACCCTCTCAGGCCAGC	3176
	GCTGGCCTGAGAGGGTCGACTCCTCAGATATGTACTGCTTCCGGATGGAATAGAACATAGCGCATTCTTTACTGAGGCTTTCAAAACATTCCTTTTCTTCGTCCCAATTCACCTGGTCCAA	3177
	AAGAATGCGCTATGTTC	3178
	GAACATAGCGCATTCTT	3179
Non-polyposis colorectal cancer Trp712Term TGG-TAG	AGGCTTATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTGCCTCCTAA	3180
	TTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTCTGGAAAACACATTAGATGTCATAAGCCT	3181
	AAACTCCTGGAAGTGGA	3182
	TCCACTTCCAGGAGTTT	3183
Non-polyposis colorectal cancer Trp714Term TGG-TAG	ATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTGCCTCCTAAACATTT	3184
	AAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTCTGGAAAACACATTAGATGTCAT	3185
	CTGGAAGTGGACTGTGG	3186
	CCACAGTCCACTTCCAG	3187
Non-polyposis colorectal cancer Trp714Term TGG-TGA	TGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAAACTCCTGGAAGTGGACTGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTGCCTCCTAAACATTTC	3188

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATGTGTTCCACAGT**C**CACTTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTCTGGAAAACACATTAGATGTCA	3189
	TGGAAGTG**G**ACTGTGGA	3190
	TCCACAGT**C**CACTTCCA	3191
Non-polyposis colorectal cancer Val716Met GTG-ATG	ATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAAACTCCTGGAAGTGGACT**G**TGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTGCCTCCTAAACATTTCACAG	3192
	CTGTGAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATGTGTTCCA**C**AGTCCACTTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTCTGGAAAACACATTAGAT	3193
	AGTGGACT**G**TGGAACAC	3194
	GTGTTCCA**C**AGTCCACT	3195
Non-polyposis colorectal cancer Tyr721Term TAT-TAA	GAGTGAAGTGCCTGGCTCCATTCCAAACTCCTGGAAGTGGACTGTGGAACACATTGTCTA**T**AAAGCCTTGCGCTCACACATTCTGCCTCCTAAACATTTCACAGAAGATGGAAATATCCTG	3196
	CAGGATATTTCCATCTTCTGTGAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTT**A**TAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTC	3197
	ATTGTCTA**T**AAAGCCTT	3198
	AAGGCTTT**A**TAGACAAT	3199
Non-polyposis colorectal cancer Lys751Arg AAA-AGA	CTAAACATTTCACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTGCCTGATCTATACA**A**AGTCTTTGAGAGGTGTTAAATATGGTTATTTATGCACTGTGGGATGTGTTCTTCTTTCTC	3200
	GAGAAAGAAGAACACATCCCACAGTGCATAAATAACCATATTTAACACCTCTCAAAGACT**T**TGTATAGATCAGGCAGGTTAGCAAGCTGCAGGATATTTCCATCTTCTGTGAAATGTTTAG	3201
	TCTATACA**A**AGTCTTTG	3202
	CAAAGACT**T**TGTATAGA	3203
Non-polyposis colorectal cancer Arg755Trp AGG-TGG	ACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTGCCTGATCTATACAAAGTCTTTGAG**A**GGTGTTAAATATGGTTATTTATGCACTGTGGGATGTGTTCTTCTTTCTCTGTATTCCGAT	3204
	ATCGGAATACAGAGAAAGAAGAACACATCCCACAGTGCATAAATAACCATATTTAACACC**T**CTCAAAGACTTTGTATAGATCAGGCAGGTTAGCAAGCTGCAGGATATTTCCATCTTCTGT	3205
	TCTTTGAG**A**GGTGTTAA	3206
	TTAACACC**T**CTCAAAGA	3207

EXAMPLE 18
Human mismatch repair - MSH2

The human MSH2 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH2 gene have been identified in a variety of cancers, including, for

example, ovarian tumors, colorectal cancer, endometrial cancer, uterine cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH2 oligonucleotides of the invention.

Table 25
MSH2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Gln252Term CAG-TAG	TTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGA AAGGCAAAAAGGGAGAG**C**AGATGAATAGTGCTGTATTGCCAG AAATGGAGAATCAGGTACATGGATTATAAATGTGAA	3208
	TTCACATTTATAATCCATGTACCTGATTCTCCATTTCTGGCAAT ACAGCACTATTCATCT**G**CTCTCCCTTTTTGCCTTTCAACAACC GGTTGAGGTCCTGATAAATGTCTTTTGTGGAAAA	3209
	AGGGAGAG**C**AGATGAAT	3210
	ATTCATCT**G**CTCTCCCT	3211
Non polyposis colorectal cancer Gln288Term CAG-TAG	TCATCACTGTCTGCGGTAATCAAGTTTTTAGAACTCTTATCAG ATGATTCCAACTTTGGA**C**AGTTTGAACTGACTACTTTTGACTT CAGCCAGTATATGAAATTGGATATTGCAGCAGTCA	3212
	TGACTGCTGCAATATCCAATTTCATATACTGGCTGAAGTCAAA AGTAGTCAGTTCAAACT**G**TCCAAAGTTGGAATCATCTGATAAG AGTTCTAAAAACTTGATTACCGCAGACAGTGATGA	3213
	ACTTTGGA**C**AGTTTGAA	3214
	TTCAAACT**G**TCCAAAGT	3215
Non polyposis colorectal cancer Ala305Thr GCA-ACA	AACTTTGGACAGTTTGAACTGACTACTTTTGACTTCAGCCAGT ATATGAAATTGGATATT**G**CAGCAGTCAGAGCCCTTAACCTTTT TCAGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAGG	3216
	CCTTTTTTTTTTTTTTTTTTTTTTTTTTTACCTGAAAAAGGTTAAG GGCTCTGACTGCTG**C**AATATCCAATTTCATATACTGGCTGAAG TCAAAAGTAGTCAGTTCAAACTGTCCAAAGTT	3217
	TGGATATT**G**CAGCAGTC	3218
	GACTGCTG**C**AATATCCA	3219
Non polyposis colorectal cancer Gly322Asp GGC-GAC	AGCTTGCCATTCTTTCTATTTTATTTTTTGTTTACTAGGGTTCT GTTGAAGATACCACTG**G**CTCTCAGTCTCTGGCTGCCTTGCTG AATAAGTGTAAAACCCCTCAAGGACAAAGACTTGT	3220
	ACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCAAGG CAGCCAGAGACTGAGAG**C**CAGTGGTATCTTCAACAGAACCCT AGTAAACAAAAAATAAAATAGAAAGAATGGCAAGCT	3221
	TACCACTG**G**CTCTCAGT	3222
	ACTGAGAG**C**CAGTGGTA	3223
Non polyposis colorectal cancer Ser323Cys TCT-TGT	TTGCCATTCTTTCTATTTTATTTTTTGTTTACTAGGGTTCTGTTG AAGATACCACTGGCT**C**TCAGTCTCTGGCTGCCTTGCTGAATA AGTGTAAAACCCCTCAAGGACAAAGACTTGTTAA	3224
	TTAACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCA AGGCAGCCAGAGACTGA**G**AGCCAGTGGTATCTTCAACAGAAC CCTAGTAAACAAAAAATAAAATAGAAAGAATGGCAA	3225

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACTGGCT**C**TCAGTCTC	3226
	GAGACTGA**G**AGCCAGTG	3227
Non polyposis colorectal cancer Arg383Term CGA-TGA	GTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTA CAAGAAGATTTACTTCGT**C**GATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACTTACAAG	3228
	CTTGTAAGTTTGCTGCTTGTCTTTGAAACTTCTTGGCAAGTCG GTTAAGATCTGGGAATC**G**ACGAAGTAAATCTTCTTGTAAAGTC TGCCTCAATTCTGCATCTTCTACAAAAGCTTCCAC	3229
	TACTTCGT**C**GATTCCCA	3230
	TGGGAATC**G**ACGAAGTA	3231
Non polyposis colorectal cancer Gln397Term CAA-TAA	CAAGAAGATTTACTTCGTCGATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGA**C**AAGCAGCAAACTTACAAGATTGTTA CCGACTCTATCAGGGTATAAATCAACTACCTAATG	3232
	CATTAGGTAGTTGATTTATACCCTGATAGAGTCGGTAACAATC TTGTAAGTTTGCTGCTT**G**TCTTTGAAACTTCTTGGCAAGTCGG TTAAGATCTGGGAATCGACGAAGTAAATCTTCTTG	3233
	TTCAAAGA**C**AAGCAGCA	3234
	TGCTGCTT**G**TCTTTGAA	3235
Non polyposis colorectal cancer Arg406Term CGA-TGA	GATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCA AACTTACAAGATTGTTAC**C**GACTCTATCAGGGTATAAATCAAC TACCTAATGTTATACAGGCTCTGGAAAAACATGAAG	3236
	CTTCATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTT ATACCCTGATAGAGTC**G**GTAACAATCTTGTAAGTTTGCTGCTT GTCTTTGAAACTTCTTGGCAAGTCGGTTAAGATC	3237
	ATTGTTAC**C**GACTCTAT	3238
	ATAGAGTC**G**GTAACAAT	3239
Non polyposis colorectal cancer Gln419Term CAG-TAG	GCAAACTTACAAGATTGTTACCGACTCTATCAGGGTATAAATC AACTACCTAATGTTATA**C**AGGCTCTGGAAAAACATGAAGGTAA CAAGTGATTTTGTTTTTTTGTTTTCCTTCAACTCA	3240
	TGAGTTGAAGGAAAACAAAAAAACAAAATCACTTGTTACCTTC ATGTTTTTCCAGAGCCT**G**TATAACATTAGGTAGTTGATTTATAC CCTGATAGAGTCGGTAACAATCTTGTAAGTTTGC	3241
	ATGTTATA**C**AGGCTCTG	3242
	CAGAGCCT**G**TATAACAT	3243
Non polyposis colorectal cancer Gln429Term CAG-TAG	TATTCTGTAAAATGAGATCTTTTTATTTGTTTGTTTTACTACTTT CTTTTAGGAAAACAC**C**AGAAATTATTGTTGGCAGTTTTTGTGA CTCCTCTTACTGATCTTCGTTCTGACTTCTCCA	3244
	TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAGTCACAAAAA CTGCCAACAATAATTTCT**G**GTGTTTTCCTAAAAGAAAGTAGTA AAACAAACAAATAAAAAGATCTCATTTTACAGAATA	3245
	GAAAACAC**C**AGAAATTA	3246
	TAATTTCT**G**GTGTTTTC	3247

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Leu458Term TTA-TGA	CTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGAAATGATAGAAACAACTT**T**AGATATGGATCAGGTATGCAATATACTTTTTAATTTAAGCAGTAGTTATTTTTAAAAAGC	3248
	GCTTTTTAAAAATAACTACTGCTTAAATTAAAAAGTATATTGCATACCTGATCCATATCT**A**AAGTTGTTTCTATCATTTCCTGAAACTTGGAGAAGTCAGAACGAAGATCAGTAAGAGGAG	3249
	AACAACTT**T**AGATATGG	3250
	CCATATCT**A**AAGTTGTT	3251
Non polyposis colorectal cancer Gln518Term CAG-TAG	TTTCTTCTTGATTATCAAGGCTTGGACCCTGGCAAACAGATTAAACTGGATTCCAGTGCA**C**AGTTTGGATATTACTTTCGTGTAACCTGTAAGGAAGAAAAAGTCCTTCGTAACAATAAAA	3252
	TTTTATTGTTACGAAGGACTTTTTCTTCCTTACAGGTTACACGAAAGTAATATCCAAACT**G**TGCACTGGAATCCAGTTTAATCTGTTTGCCAGGGTCCAAGCCTTGATAATCAAGAAGAAA	3253
	CCAGTGCA**C**AGTTTGGA	3254
	TCCAAACT**G**TGCACTGG	3255
Non polyposis colorectal cancer Arg524Pro CGT-CCT	GCTTGGACCCTGGCAAACAGATTAAACTGGATTCCAGTGCACAGTTTGGATATTACTTTC**G**TGTAACCTGTAAGGAAGAAAAAGTCCTTCGTAACAATAAAAACTTTAGTACTGTAGATAT	3256
	ATATCTACAGTACTAAAGTTTTTATTGTTACGAAGGACTTTTTCTTCCTTACAGGTTACA**C**GAAAGTAATATCCAAACTGTGCACTGGAATCCAGTTTAATCTGTTTGCCAGGGTCCAAGC	3257
	TTACTTTC**G**TGTAACCT	3258
	AGGTTACA**C**GAAAGTAA	3259
Non polyposis colorectal cancer Glu562Val GAG-GTG	TTAATATTTTTAATAAAACTGTTATTTCGATTTGCAGCAAATTGACTTCTTTAAATGAAG**A**GTATACCAAAAATAAAACAGAATATGAAGAAGCCCAGGATGCCATTGTTAAAGAAATTGT	3260
	ACAATTTCTTTAACAATGGCATCCTGGGCTTCTTCATATTCTGTTTTATTTTTGGTATAC**T**CTTCATTTAAAGAAGTCAATTTGCTGCAAATCGAAATAACAGTTTTATTAAAAATATTAA	3261
	AAATGAAG**A**GTATACCA	3262
	TGGTATAC**T**CTTCATTT	3263
Glioma Glu580Term GAA-TAA	AATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCCAGGATGCCATTGTTAAA**G**AAATTGTCAATATTTCTTCAGGTAAACTTAATAGAACTAATAATGTTCTGAATGTCACCT	3264
	AGGTGACATTCAGAACATTATTAGTTCTATTAAGTTTACCTGAAGAAATATTGACAATTT**C**TTTAACAATGGCATCCTGGGCTTCTTCATATTCTGTTTTATTTTTGGTATACTCTTCATT	3265
	TTGTTAAA**G**AAATTGTC	3266
	GACAATTT**C**TTTAACAA	3267
Non polyposis colorectal cancer Gln601Term CAG-TAG	TGTTTTTATTTTTATACAGGCTATGTAGAACCAATGCAGACACTCAATGATGTGTTAGCT**C**AGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCACCTGTTCCATATGTAC	3268

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTACATATGGAACAGGTGCTCCATTTGACACGTGAGCAAAGC TGACAACAGCATCTAGCT**G**AGCTAACACATCATTGAGTGTCTG CATTGGTTCTACATAGCCTGTATAAAAATAAAAACA	3269
	TGTTAGCT**C**AGCTAGAT	3270
	ATCTAGCT**G**AGCTAACA	3271
Non polyposis colorectal cancer Tyr619Term TAT-TAG	AGCTCAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAAT GGAGCACCTGTTCCATA**T**GTACGACCAGCCATTTTGGAGAAA GGACAAGGAAGAATTATATTAAAAGCATCCAGGCAT	3272
	ATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTCTCCA AAATGGCTGGTCGTAC**A**TATGGAACAGGTGCTCCATTTGACA CGTGAGCAAAGCTGACAACAGCATCTAGCTGAGCT	3273
	GTTCCATA**T**GTACGACC	3274
	GGTCGTAC**A**TATGGAAC	3275
Non polyposis colorectal cancer Arg621Term CGA-TGA	CAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGA GCACCTGTTCCATATGTA**C**GACCAGCCATTTTGGAGAAAGGA CAAGGAAGAATTATATTAAAAGCATCCAGGCATGCTT	3276
	AAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTC TCCAAAATGGCTGGTC**G**TACATATGGAACAGGTGCTCCATTT GACACGTGAGCAAAGCTGACAACAGCATCTAGCTG	3277
	CATATGTA**C**GACCAGCC	3278
	GGCTGGTC**G**TACATATG	3279
Non polyposis colorectal cancer Pro622Leu CCA-CTA	TAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCAC CTGTTCCATATGTACGAC**C**AGCCATTTTGGAGAAAGGACAAG GAAGAATTATATTAAAAGCATCCAGGCATGCTTGTGT	3280
	ACACAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTC CTTTCTCCAAAATGGCT**G**GTCGTACATATGGAACAGGTGCTC CATTTGACACGTGAGCAAAGCTGACAACAGCATCTA	3281
	TGTACGAC**C**AGCCATTT	3282
	AAATGGCT**G**GTCGTACA	3283
Non polyposis colorectal cancer Ala636Pro GCA-CCA	CCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAA GGAAGAATTATATTAAAA**G**CATCCAGGCATGCTTGTGTTGAAG TTCAAGATGAAATTGCATTTATTCCTAATGACGTAT	3284
	ATACGTCATTAGGAATAAATGCAATTTCATCTTGAACTTCAACA CAAGCATGCCTGGATG**C**TTTTAATATAATTCTTCCTTGTCCTTT CTCCAAAATGGCTGGTCGTACATATGGAACAGG	3285
	TATTAAAA**G**CATCCAGG	3286
	CCTGGATG**C**TTTTAATA	3287
Non polyposis colorectal cancer His639Arg CAT-CGT	ATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATTA TATTAAAAGCATCCAGGC**A**TGCTTGTGTTGAAGTTCAAGATGA AATTGCATTTATTCCTAATGACGTATACTTTGAAAA	3288
	TTTTCAAAGTATACGTCATTAGGAATAAATGCAATTTCATCTTG AACTTCAACACAAGCA**T**GCCTGGATGCTTTTAATATAATTCTTC CTTGTCCTTTCTCCAAAATGGCTGGTCGTACAT	3289
	ATCCAGGC**A**TGCTTGTG	3290

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CACAAGCA**T**GCCTGGAT	3291
Non polyposis colorectal cancer His639Tyr CAT-TAT	TATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATTATATTAAAAGCATCCAGG**C**ATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTAATGACGTATACTTTGAAA	3292
	TTTCAAAGTATACGTCATTAGGAATAAATGCAATTTCATCTTGAACTTCAACACAAGCAT**G**CCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTCTCCAAAATGGCTGGTCGTACATA	3293
	CATCCAGG**C**ATGCTTGT	3294
	ACAAGCAT**G**CCTGGATG	3295
Non polyposis colorectal cancer Glu647Lys GAA-AAA	AAAGGACAAGGAAGAATTATATTAAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGAT**G**AAATTGCATTTATTCCTAATGACGTATACTTTGAAAAAGATAAACAGATGTTCCACATCA	3296
	TGATGTGGAACATCTGTTTATCTTTTTCAAAGTATACGTCATTAGGAATAAATGCAATTT**C**ATCTTGAACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTT	3297
	TTCAAGAT**G**AAATTGCA	3298
	TGCAATTT**C**ATCTTGAA	3299
Non polyposis colorectal cancer Tyr656Term TAC-TAG	ATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTAATGACGTATA**C**TTTGAAAAAGATAAACAGATGTTCCACATCATTACTGGTAAAAAACCTGGTTTTTGGGCT	3300
	AGCCCAAAAACCAGGTTTTTACCAGTAATGATGTGGAACATCTGTTTATCTTTTTCAAA**G**TATACGTCATTAGGAATAAATGCAATTTCATCTTGAACTTCAACACAAGCATGCCTGGAT	3301
	GACGTATA**C**TTTGAAAA	3302
	TTTTCAAA**G**TATACGTC	3303
Non polyposis colorectal cancer Gly674Asp GGT-GAT	GAAAGAAGTTTAAAATCTTGCTTTCTGATATAATTTGTTTTGTAGGCCCCAATATGGGAG**G**TAAATCAACATATATTCGACAAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTT	3304
	AAACACCCAATTTGGGCCATGAGTACTATCACCCCAGTTTGTCGAATATATGTTGATTTA**C**CTCCCATATTGGGGCCTACAAAACAAATTATATCAGAAAGCAAGATTTTAAACTTCTTTC	3305
	TATGGGAG**G**TAAATCAA	3306
	TTGATTTA**C**CTCCCATA	3307
Non polyposis colorectal cancer Arg680Term CGA-TGA	TTGCTTTCTGATATAATTTGTTTTGTAGGCCCCAATATGGGAGGTAAATCAACATATATT**C**GACAAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCAG	3308
	CTGACTCACATGGCACAAAACACCCAATTTGGGCCATGAGTACTATCACCCCAGTTTGTC**G**AATATATGTTGATTTACCTCCCATATTGGGGCCTACAAAACAAATTATATCAGAAAGCAA	3309
	CATATATT**C**GACAAACT	3310
	AGTTTGTC**G**AATATATG	3311

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non polyposis colorectal cancer Gly692Arg GGG-CGG	ATGGGAGGTAAATCAACATATATTCGACAAACTGGGGTGATAGTACTCATGGCCCAAATT**G**GGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGAG	3312
	CTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACTCACATGGCACAAAACACC**C**AATTTGGGCCATGAGTACTATCACCCCAGTTTGTCGAATATATGTTGATTTACCTCCCAT	3313
	CCCAAATT**G**GGTGTTTT	3314
	AAAACACC**C**AATTTGGG	3315
Non polyposis colorectal cancer Cys697Arg TGT-CGT	ACATATATTCGACAAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTTTGTGCCA**T**GTGAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACA	3316
	TGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACTCAC**A**TGGCACAAAACACCCAATTTGGGCCATGAGTACTATCACCCCAGTTTGTCGAATATATGT	3317
	TTGTGCCA**T**GTGAGTCA	3318
	TGACTCAC**A**TGGCACAA	3319
Non polyposis colorectal cancer Cys697Phe TGT-TTT	CATATATTCGACAAACTGGGGTGATAGTACTCATGGCCCAAATTGGGTGTTTTGTGCCAT**G**TGAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAG	3320
	CTGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACTCA**C**ATGGCACAAAACACCCAATTTGGGCCATGAGTACTATCACCCCAGTTTGTCGAATATATG	3321
	TGTGCCAT**G**TGAGTCAG	3322
	CTGACTCA**C**ATGGCACA	3323
Non polyposis colorectal cancer Gln718Term CAA-TAA	GAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAGT**C**AATTGAAAGGAGTCTCCACGTTCATGGCTGAAATGTTGGAAACTGCTTCTATCCTCAGGT	3324
	ACCTGAGGATAGAAGCAGTTTCCAACATTTCAGCCATGAACGTGGAGACTCCTTTCAATT**G**ACTGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACTC	3325
	GTGACAGT**C**AATTGAAA	3326
	TTTCAATT**G**ACTGTCAC	3327
Non polyposis colorectal cancer Leu811Term TTA-TGA	CCAATCAGATACCAACTGTTAATAATCTACATGTCACAGCACTCACCACTGAAGAGACCT**T**AACTATGCTTTATCAGGTGAAGAAAGGTATGTACTATTGGAGTACTCTAAATTCAGAACT	3328
	AGTTCTGAATTTAGAGTACTCCAATAGTACATACCTTTCTTCACCTGATAAAGCATAGTT**A**AGGTCTCTTCAGTGGTGAGTGCTGTGACATGTAGATTATTAACAGTTGGTATCTGATTGG	3329
	AGAGACCT**T**AACTATGC	3330
	GCATAGTT**A**AGGTCTCT	3331
Non polyposis colorectal cancer Ala834Thr GCT-ACT	TTCCCCAAATTTCTTATAGGTGTCTGTGATCAAAGTTTTGGGATTCATGTTGCAGAGCTT**G**CTAATTTCCCTAAGCATGTAATAGAGTGTGCTAAACAGAAAGCCCTGGAACTTGAGGAGT	3332

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTCCTCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTATTAC ATGCTTAGGGAAATTAG**C**AAGCTCTGCAACATGAATCCCAAAA CTTTGATCACAGACACCTATAAGAAATTTGGGGAA	3333
	CAGAGCTT**G**CTAATTTC	3334
	GAAATTAG**C**AAGCTCTG	3335
Non polyposis colorectal cancer Gln861Term CAA-TAA	ATAGAGTGTGCTAAACAGAAAGCCCTGGAACTTGAGGAGTTT CAGTATATTGGAGAATCG**C**AAGGATATGATATCATGGAACCAG CAGCAAAGAAGTGCTATCTGGAAAGAGAGGTTTGTC	3336
	GACAAACCTCTCTTTCCAGATAGCACTTCTTTGCTGCTGGTTC CATGATATCATATCCTT**G**CGATTCTCCAATATACTGAAACTCCT CAAGTTCCAGGGCTTTCTGTTTAGCACACTCTAT	3337
	GAGAATCG**C**AAGGATAT	3338
	ATATCCTT**G**CGATTCTC	3339
Non polyposis colorectal cancer Thr905Arg ACA-AGA	AGGAGTTCCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAAT GTCAGAAGAAAACATCA**C**AATAAAGTTAAAACAGCTAAAAGCT GAAGTAATAGCAAAGAATAATAGCTTTGTAAATGA	3340
	TCATTTACAAAGCTATTATTCTTTGCTATTACTTCAGCTTTTAG CTGTTTTAACTTTATT**G**TGATGTTTTCTTCTGACATTTCAGTAA AGGGCATTTGTTTCACCTTGGACAGGAACTCCT	3341
	AAACATCA**C**AATAAAGT	3342
	ACTTTATT**G**TGATGTTT	3343

EXAMPLE 19
Human mismatch repair - MSH6

The human MSH6 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH6 gene have been identified in a variety of cancers, including particularly hereditary nonpolyposis colorectal cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH6 oligonucleotides of the invention.

Table 26
MSH6 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Non-polyposis colorectal cancer Ser144Ile AGC-ATC	GGAAATCAGTCCGTGTTCATGTACAGTTTTTTGATGACAGCCC AACAAGGGGCTGGGTTA**G**CAAAAGGCTTTTAAAGCCATATAC AGGTAAGAGTCACTACTGCCATGTGTGTGTGTTTGT	3344

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAAACACACACACATGGCAGTAGTGACTCTTACCTGTATATG GCTTTAAAAGCCTTTTG**C**TAACCCAGCCCCTTGTTGGGCTGT CATCAAAAAACTGTACATGAACACGGACTGATTTCC	3345
	CTGGGTTA**G**CAAAAGGC	3346
	GCCTTTTG**C**TAACCCAG	3347
Endometrial cancer Ser156Term TCA-TGA	CGTGAGCCTCTGCACCCGGCCCTTATTGTTTATAAATACATTT CTTTCTAGGTTCAAAAT**C**AAAGGAAGCCCAGAAGGGAGGTCA TTTTTACAGTGCAAAGCCTGAAATACTGAGAGCAAT	3348
	ATTGCTCTCAGTATTTCAGGCTTTGCACTGTAAAAATGACCTC CCTTCTGGGCTTCCTTT**G**ATTTTGAACCTAGAAAGAAATGTAT TTATAAACAATAAGGGCCGGGTGCAGAGGCTCACG	3349
	TTCAAAAT**C**AAAGGAAG	3350
	CTTCCTTT**G**ATTTTGAA	3351
Early onset colorectal cancer Tyr214Term TAC-TAG	TTCCAAATTTTGATTTGTTTTTAAATACTCTTTCCTTGCCTGGC AGGTAGGCACAACTTA**C**GTAACAGATAAGAGTGAAGAAGATA ATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAG	3352
	CTTAGGCTGTACTTCCTCTTCACTCTCAATTTCATTATCTTCTT CACTCTTATCTGTTAC**G**TAAGTTGTGCCTACCTGCCAGGCAA GGAAAGAGTATTTAAAAACAAATCAAAATTTGGAA	3353
	ACAACTTA**C**GTAACAGA	3354
	TCTGTTAC**G**TAAGTTGT	3355
Endometrial cancer Arg248Term CGA-TGA	GAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGT AGCCGCCAAATAAAAAAA**C**GAAGGGTCATATCAGATTCTGAG AGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAG	3356
	CTGGCTTAAATTCCACATCAGAGCCACCAATGTCACTCTCAGA ATCTGATATGACCCTTC**G**TTTTTTTATTTGGCGGCTACTTCGC CTAGATCCTTGTGTCTTAGGCTGTACTTCCTCTTC	3357
	TAAAAAAA**C**GAAGGGTC	3358
	GACCCTTC**G**TTTTTTTA	3359
Colorectal cancer Ser285Ile AGT-ATT	TTAAGCCAGACACTAAGGAGGAAGGAAGCAGTGATGAAATAA GCAGTGGAGTGGGGGATA**G**TGAGAGTGAAGGCCTGAACAGC CCTGTCAAAGTTGCTCGAAAGCGGAAGAGAATGGTGAC	3360
	GTCACCATTCTCTTCCGCTTTCGAGCAACTTTGACAGGGCTG TTCAGGCCTTCACTCTCA**C**TATCCCCCACTCCACTGCTTATTT CATCACTGCTTCCTTCCTCCTTAGTGTCTGGCTTAA	3361
	GGGGGATA**G**TGAGAGTG	3362
	CACTCTCA**C**TATCCCCC	3363
Colorectal cancer Gly566Arg GGA-AGA	GAGGAAGATTCTTCTGGCCATACTCGTGCATATGGTGTGTGC TTTGTTGATACTTCACTG**G**GAAAGTTTTTCATAGGTCAGTTTTC AGATGATCGCCATTGTTCGAGATTTAGGACTCTAG	3364

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTAGAGTCCTAAATCTCGAACAATGGCGATCATCTGAAAACTG ACCTATGAAAAACTTTC**C**CAGTGAAGTATCAACAAAGCACACA CCATATGCACGAGTATGGCCAGAAGAATCTTCCTC	3365
	CTTCACTG**G**GAAAGTTT	3366
	AAACTTTC**C**CAGTGAAG	3367
Non-polyposis colorectal cancer Gln698Glu CAG-GAG	GAATTGGCCCTCTCTGCTCTAGGTGGTTGTGTCTTCTACCTC AAAAAATGCCTTATTGAT**C**AGGAGCTTTTATCAATGGCTAATTT TGAAGAATATATTCCCTTGGATTCTGACACAGTCA	3368
	TGACTGTGTCAGAATCCAAGGGAATATATTCTTCAAAATTAGC CATTGATAAAAGCTCCT**G**ATCAATAAGGCATTTTTTGAGGTAG AAGACACAACCACCTAGAGCAGAGAGGGCCAATTC	3369
	TTATTGAT**C**AGGAGCTT	3370
	AAGCTCCT**G**ATCAATAA	3371
Endometrial cancer Gln731Term CAA-TAA	CCCTTGGATTCTGACACAGTCAGCACTACAAGATCTGGTGCT ATCTTCACCAAAGCCTAT**C**AACGAATGGTGCTAGATGCAGTG ACATTAAACAACTTGGAGATTTTTCTGAATGGAACAA	3372
	TTGTTCCATTCAGAAAAATCTCCAAGTTGTTTAATGTCACTGCA TCTAGCACCATTCGTT**G**ATAGGCTTTGGTGAAGATAGCACCA GATCTTGTAGTGCTGACTGTGTCAGAATCCAAGGG	3373
	AAGCCTAT**C**AACGAATG	3374
	CATTCGTT**G**ATAGGCTT	3375
Colorectal cancer Val800Leu GTT-CTT	GCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATG CCATAGAAGACCTCATG**G**TTGTGCCTGACAAAATCTCCGAAG TTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGA	3376
	TCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTACAACTTCGGA GATTTTGTCAGGCACAA**C**CATGAGGTCTTCTATGGCATCTAGA CGATCATTAATAGCATAATGGTTACAGAGTGGGGC	3377
	ACCTCATG**G**TTGTGCCT	3378
	AGGCACAA**C**CATGAGGT	3379
Colorectal cancer Asp803Gly GAC-GGC	GTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAAGA CCTCATGGTTGTGCCTG**A**CAAAATCTCCGAAGTTGTAGAGCT TCTAAAGAAGCTTCCAGATCTTGAGAGGCTACTCAG	3380
	CTGAGTAGCCTCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTA CAACTTCGGAGATTTTG**T**CAGGCACAACCATGAGGTCTTCTAT GGCATCTAGACGATCATTAATAGCATAATGGTTAC	3381
	TGTGCCTG**A**CAAAATCT	3382
	AGATTTTG**T**CAGGCACA	3383
Non-polyposis colorectal cancer Tyr850Cys TAC-TGC	CTCCCCTGAAGAGTCAGAACCACCCAGACACCAGGGCTATAA TGTATGAAGAAACTACAT**A**CAGCAAGAAGAAGATTATTGATTT TCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAA	3384

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTACACATTACTTTGAATCCTTCCAGAGCAGAAAGAAAATCAA TAATCTTCTTCTTGCTG**T**ATGTAGTTTCTTCATACATTATAGCC CTGCTGTCTGGGTGGTTCTGACTCTTCAGGGGAG	3385
	AACTACAT**A**CAGCAAGA	3386
	TCTTGCTG**T**ATGTAGTT	3387
Colorectal cancer Pro1087Thr CCC-ACC	TATAGTCGAGGGGGTGATGGTCCTATGTGTCGCCCAGTAATT CTGTTGCCGGAAGATACC**C**CCCCCTTCTTAGAGCTTAAAGGA TCACGCCATCCTTGCATTACGAAGACTTTTTTTGGAG	3388
	CTCCAAAAAAAGTCTTCGTAATGCAAGGATGGCGTGATCCTTT AAGCTCTAAGAAGGGGG**G**GGTATCTTCCGGCAACAGAATTAC TGGGCGACACATAGGACCATCACCCCCTCGACTATA	3389
	AAGATACC**C**CCCCCTTC	3390
	GAAGGGGG**G**GGTATCTT	3391
Non-polyposis colorectal cancer Gln1258Term CAA-TAA	ACTATAAAATGTCGTACATTATTTTCAACTCACTACCATTCATT AGTAGAAGATTATTCT**C**AAAATGTTGCTGTGCGCCTAGGACAT ATGGTATGTGCAAATTGTTTTTTTCCACAAATTC	3392
	GAATTTGTGGAAAAAAACAATTTGCACATACCATATGTCCTAG GCGCACAGCAACATTTT**G**AGAATAATCTTCTACTAATGAATGG TAGTGAGTTGAAAATAATGTACGACATTTTATAGT	3393
	ATTATTCT**C**AAAATGTT	3394
	AACATTTT**G**AGAATAAT	3395

EXAMPLE 20
Hyperlipidemia - APOE

Hyperlipidemia is the abnormal elevation of plasma cholesterol and/or triglyceride levels and it is one of the most common diseases. The human apolipoprotein E protein is involved in the transport of endogenous lipids and appears to be crucial for both the direct removal of cholesterol-rich LDL from plasma and conversion of IDL particles to LDL particles. Individuals who either lack apolipoprotein E or who are homozygous for particular alleles of apoE may have have a condition known as dysbetalipoproteinemia, which is characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis.

In a comprehensive review of apoE variants, de Knijff et al., *Hum. Mutat.* 4:178-194 (1994) found that 30 variants had been characterized, including the most common variant, apoE3. To that time, 14 apoE variants had been found to be associated with familial dysbetalipoproteinemia. The

attached table discloses the correcting oligonucleotide base sequences for the APOE oligonucleotides of the invention.

Table 27
APOE Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Glu13Lys cGAG-AAG	TTGTTCCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGT GGAGACAGAGCCGGAGCCC**G**AGCTGCGCCAGCAGACCGAG TGGCAGAGCGGCCAGCGCTGGGAACTGGCACTGGGTCGCT	3396
	AGCGACCCAGTGCCAGTTCCCAGCGCTGGCCGCTCTGCCAC TCGGTCTGCTGGCGCAGCT**C**GGGCTCCGGCTCTGTCTCCAC CGCTTGCTCCACCTTGGCCTGGCATCCTGTGTGGAACAA	3397
	CGGAGCCC**G**AGCTGCGC	3398
	GCGCAGCT**C**GGGCTCCG	3399
Apolipoprotein E Trp20Term TGGc-TGA	CAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAG CTGCGCCAGCAGACCGAGTG**G**CAGAGCGGCCAGCGCTGGG AACTGGCACTGGGTCGCTTTTGGGATTACCTGCGCTGGGTG	3400
	CACCCAGCGCAGGTAATCCCAAAAGCGACCCAGTGCCAGTT CCCAGCGCTGGCCGCTCTG**C**CACTCGGTCTGCTGGCGCAGC TCGGGCTCCGGCTCTGTCTCCACCGCTTGCTCCACCTTG	3401
	ACCGAGTG**G**CAGAGCGG	3402
	CCGCTCTG**C**CACTCGGT	3403
Apolipoprotein E Leu28Pro CTG-CCG	CAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGGCA GAGCGGCCAGCGCTGGGAAC**T**GGCACTGGGTCGCTTTTGGG ATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCA	3404
	TGCACCTGCTCAGACAGTGTCTGCACCCAGCGCAGGTAATCC CAAAAGCGACCCAGTGCC**A**GTTCCCAGCGCTGGCCGCTCTG CCACTCGGTCTGCTGGCGCAGCTCGGGCTCCGGCTCTG	3405
	CTGGGAAC**T**GGCACTGG	3406
	CCAGTGCC**A**GTTCCCAG	3407
Apolipoprotein E Cys112Arg gTGC-CGC	CGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGG GCGCGGACATGGAGGACGTG**T**GCGGCCGCCTGGTGCAGTA CCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAG G	3408
	CCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGCGG TACTGCACCAGGCGGCCGC**A**CACGTCCTCCATGTCCGCGCC CAGCCGGGCCTGCGCCGCCTGCAGCTCCTTGGACAGCCG	3409
	AGGACGTG**T**GCGGCCGC	3410
	GCGGCCGC**A**CACGTCCT	3411
Apolipoprotein E Gly127Asp GGC-GAC	ACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGG CGAGGTGCAGGCCATGCTCG**G**CCAGAGCACCGAGGAGCTG CGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCG	3412

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGCACCC GCAGCTCCTCGGTGCTCTGG**C**CGAGCATGGCCTGCACCTCG CCGCGGTACTGCACCAGGCGGCCGCACACGTCCTCCATGT	3413
	CATGCTCG**G**CCAGAGCA	3414
	TGCTCTGG**C**CGAGCATG	3415
Apolipoprotein E Arg136Cys gCGC-TGC	GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTG**C**GCCTCGCCTCCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3416
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGC**G**CACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3417
	TGCGGGTG**C**GCCTCGCC	3418
	GGCGAGGC**G**CACCCGCA	3419
Apolipoprotein E Arg136His CGC-CAC	TGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAG CACCGAGGAGCTGCGGGTGC**G**CCTCGCCTCCCACCTGCGC AAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCA	3420
	TGCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTT GCGCAGGTGGGAGGCGAGG**C**GCACCCGCAGCTCCTCGGTG CTCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCA	3421
	GCGGGTGC**G**CCTCGCCT	3422
	AGGCGAGG**C**GCACCCGC	3423
Apolipoprotein E Arg136Ser gCGC-AGC	GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTG**C**GCCTCGCCTCCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC	3424
	GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGC**G**CACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC	3425
	TGCGGGTG**C**GCCTCGCC	3426
	GGCGAGGC**G**CACCCGCA	3427
Apolipoprotein E Arg142Cys gCGC-TGC	GTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGG TGCGCCTCGCCTCCCACCTG**C**GCAAGCTGCGTAAGCGGCTC CTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT	3428
	ACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAGG AGCCGCTTACGCAGCTTGC**G**CAGGTGGGAGGCGAGGCGCA CCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCAC	3429
	CCCACCTG**C**GCAAGCTG	3430
	CAGCTTGC**G**CAGGTGGG	3431
Apolipoprotein E Arg142Leu CGC-CTC	TGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGT GCGCCTCGCCTCCCACCTGC**G**CAAGCTGCGTAAGCGGCTCC TCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGTA	3432
	TACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAG GAGCCGCTTACGCAGCTTG**C**GCAGGTGGGAGGCGAGGCGC ACCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCA	3433
	CCACCTGC**G**CAAGCTGC	3434

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCAGCTTG**C**GCAGGTGG	3435
Apolipoprotein E Arg145Cys gCGT-TGT	ATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCG CCTCCCACCTGCGCAAGCTG**C**GTAAGCGGCTCCTCCGCGAT GCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG	3436
	CGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGCA TCGCGGAGGAGCCGCTTAC**G**CAGCTTGCGCAGGTGGGAGG CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCAT	3437
	GCAAGCTG**C**GTAAGCGG	3438
	CCGCTTAC**G**CAGCTTGC	3439
Apolipoprotein E Arg145Pro CGT-CCT	TGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGC CTCCCACCTGCGCAAGCTGC**G**TAAGCGGCTCCTCCGCGATG CCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGG	3440
	CCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGC ATCGCGGAGGAGCCGCTTA**C**GCAGCTTGCGCAGGTGGGAG GCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCA	3441
	CAAGCTGC**G**TAAGCGGC	3442
	GCCGCTTA**C**GCAGCTTG	3443
Apolipoprotein E Lys146Gln tAAG-CAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT CCCACCTGCGCAAGCTGCGT**A**AGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	3444
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCT**T**ACGCAGCTTGCGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	3445
	AGCTGCGT**A**AGCGGCTC	3446
	GAGCCGCT**T**ACGCAGCT	3447
Apolipoprotein E Lys146Glu tAAG-GAG	CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT CCCACCTGCGCAAGCTGCGT**A**AGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG	3448
	CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCT**T**ACGCAGCTTGCGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG	3449
	AGCTGCGT**A**AGCGGCTC	3450
	GAGCCGCT**T**ACGCAGCT	3451
Apolipoprotein E Arg158Cys gCGC-TGC	GCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGA TGCCGATGACCTGCAGAAG**C**GCCTGGCAGTGTACCAGGCCG GGGCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCC	3452
	GGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCC GGCCTGGTACACTGCCAGGC**G**CTTCTGCAGGTCATCGGCAT CGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGC	3453
	TGCAGAAG**C**GCCTGGCA	3454
	TGCCAGGC**G**CTTCTGCA	3455

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Apolipoprotein E Gln187Glu aCAG-GAG	CGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTGGTGGAA**C**AGGGCCGCGTGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGG	3456
	CCCGCTCCTGTAGCGGCTGGCCGGCCAGGGAGCCCACAGTGGCGGCCCGCACGCGGCCCT**G**TTCCACCAGGGGCCCCAGGCGCTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCG	3457
	TGGTGGAA**C**AGGGCCGC	3458
	GCGGCCCT**G**TTCCACCA	3459
Apolipoprotein E Trp210Term TGG-TAG	TGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGGGCCCAGGCCT**G**GGGCGAGCGGCTGCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGACCGCCTGGA	3460
	TCCAGGCGGTCGCGGGTCCGGCTGCCCATCTCCTCCATCCGCGCGCGCAGCCGCTCGCCC**C**AGGCCTGGGCCCGCTCCTGTAGCGGCTGGCCGGCCAGGGAGCCCACAGTGGCGGCCCGCA	3461
	CCAGGCCT**G**GGGCGAGC	3462
	GCTCGCCC**C**AGGCCTGG	3463
Apolipoprotein E Arg228Cys cCGC-TGC	CAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGATGGGCAGCCGGACCCGCGAC**C**GCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAGGCCC	3464
	GGGCCTGCTCCTCCAGCTTGGCGCGCACCTCCGCCACCTGCTCCTTCACCTCGTCCAGGC**G**GTCGCGGGTCCGGCTGCCCATCTCCTCCATCCGCGCGCGCAGCCGCTCGCCCCAGGCCTG	3465
	CCCGCGAC**C**GCCTGGAC	3466
	GTCCAGGC**G**GTCGCGGG	3467
Apolipoprotein E Glu244Lys gGAG-AAG	CGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGCGCCAAGCTG**G**AGGAGCAGGCCCAGCAGATACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCT	3468
	AGCTCTTGAGGCGGGCCTGGAAGGCCTCGGCCTGCAGGCGTATCTGCTGGGCCTGCTCCT**C**CAGCTTGGCGCGCACCTCCGCCACCTGCTCCTTCACCTCGTCCAGGCGGTCGCGGGTCCG	3469
	CCAAGCTG**G**AGGAGCAG	3470
	CTGCTCCT**C**CAGCTTGG	3471

EXAMPLE 21
Familial hypercholesterolemia - LDLR

Familial hypercholesterolemia is characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL) and is, hence, one of the conditions producing a hyperlipoproteinemia phenotype. Familial hypercholesterolemia is an autosomal dominant disorder characterized by elevation

of serum cholesterol bound to low density lipoprotein (LDL). Mutations in the LDL receptor (LDLR) gene cause this disorder. The attached table discloses the correcting oligonucleotide base sequences for the LDLR oligonucleotides of the invention.

Table 28
LDLR Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu10Term cGAG-TAG	GCGTTGAGAGACCCTTTCTCCTTTTCCTCTCTCTCAGTGGGC GACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGGAA ATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTG	3472
	CAGCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCC CGTCTTGGCACTGGAACTCGTTTCTTTCGCATCTGTCGCCCA CTGAGAGAGAGGAAAAGGAGAAAGGGTCTCTCAACGC	3473
	AAAGAAACGAGTTCCAG	3474
	CTGGAACTCGTTTCTTT	3475
Hypercholesterolaemia Gln12Term cCAG-TAG	AGAGACCCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGA TGCGAAAGAAACGAGTTCCAGTGCCAAGACGGGAAATGCATC TCCTACAAGTGGGTCTGCGATGGCAGCGCTGAGTGCC	3476
	GGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGGAGATG CATTTCCCGTCTTGGCACTGGAACTCGTTTCTTTCGCATCTGT CGCCCACTGAGAGAGAGGAAAAGGAGAAAGGGTCTCT	3477
	ACGAGTTCCAGTGCCAA	3478
	TTGGCACTGGAACTCGT	3479
Hypercholesterolaemia Gln14Term cCAA-TAA	CCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGATGCGAA AGAAACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTAC AAGTGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATG	3480
	CATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTTGTAG GAGATGCATTTCCCGTCTTGGCACTGGAACTCGTTTCTTTCG CATCTGTCGCCCACTGAGAGAGAGGAAAAGGAGAAAGG	3481
	TCCAGTGCCAAGACGGG	3482
	CCCGTCTTGGCACTGGA	3483
Hypercholesterolaemia Trp23Term TGG-TAG	GCGACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGG AAATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTGAG TGCCAGGATGGCTCTGATGAGTCCCAGGAGACGTGCTG	3484
	CAGCACGTCTCCTGGGACTCATCAGAGCCATCCTGGCACTCA GCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCCCG TCTTGGCACTGGAACTCGTTTCTTTCGCATCTGTCGC	3485
	CTACAAGTGGGTCTGCG	3486
	CGCAGACCCACTTGTAG	3487
Hypercholesterolaemia Ala29Ser cGCT-TCT	AACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTACAAG TGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGA TGAGTCCCAGGAGACGTGCTGTGAGTCCCCTTTGGGCA	3488

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGCCCAAAGGGGACTCACAGCACGTCTCCTGGGACTCATCA GAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTT GTAGGAGATGCATTTCCCGTCTTGGCACTGGAACTCGTT	3489
	ATGGCAGCGCTGAGTGC	3490
	GCACTCAGCGCTGCCAT	3491
Hypercholesterolaemia Cys31Tyr TGC-TAC	TCCAGTGCCAAGACGGGAAATGCATCTCCTACAAGTGGGTCT GCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGATGAGTCC CAGGAGACGTGCTGTGAGTCCCCTTTGGGCATGATATG	3492
	CATATCATGCCCAAAGGGGACTCACAGCACGTCTCCTGGGAC TCATCAGAGCCATCCTGGCACTCAGCGCTGCCATCGCAGAC CCACTTGTAGGAGATGCATTTCCCGTCTTGGCACTGGA	3493
	CGCTGAGTGCCAGGATG	3494
	CATCCTGGCACTCAGCG	3495
Hypercholesterolaemia Arg57Cys cCGT-TGT	AATCCTGTCTCTTCTGTAGTGTCTGTCACCTGCAAATCCGGG GACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCATTCCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACG	3496
	CGTTGTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAG GAATGCAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCG GATTTGCAGGTGACAGACACTACAGAAGAGACAGGATT	3497
	GTGGGGGCCGTGTCAAC	3498
	GTTGACACGGCCCCCAC	3499
Hypercholesterolaemia Gln64Term tCAG-TAG	TCTGTCACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCG TGTCAACCGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCA AGTGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTC	3500
	GACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCACTTGGC CATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGACACGG CCCCCACAGCTGAAGTCCCCGGATTTGCAGGTGACAGA	3501
	GCATTCCTCAGTTCTGG	3502
	CCAGAACTGAGGAATGC	3503
Hypercholesterolaemia Trp66Gly cTGG-GGG	ACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAA CCGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGG ACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGT	3504
	ACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCA CTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGGT	3505
	CTCAGTTCTGGAGGTGC	3506
	GCACCTCCAGAACTGAG	3507
Hypercholesterolaemia Trp66Term TGG-TAG	CCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAAC CGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTG	3508
	CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGG	3509
	TCAGTTCTGGAGGTGCG	3510

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCACCTC**C**AGAACTGA	3511
Hypercholesterolaemia Cys68Arg gTGC-CGC	AAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTG CATTCCTCAGTTCTGGAGG**T**GCGATGGCCAAGTGGACTGCGA CAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCC	3512
	GGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGC AGTCCACTTGGCCATCGC**A**CCTCCAGAACTGAGGAATGCAG CGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATTT	3513
	TCTGGAGG**T**GCGATGGC	3514
	GCCATCGC**A**CCTCCAGA	3515
Hypercholesterolaemia Cys68Trp TGCg-TGG	ATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCA TTCCTCAGTTCTGGAGGTG**C**GATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCT	3516
	AGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC GCAGTCCACTTGGCCATC**G**CACCTCCAGAACTGAGGAATGCA GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGAT	3517
	TGGAGGTG**C**GATGGCCA	3518
	TGGCCATC**G**CACCTCCA	3519
Hypercholesterolaemia Cys68Tyr TGC-TAC	AATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGC ATTCCTCAGTTCTGGAGGT**G**CGATGGCCAAGTGGACTGCGAC AACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC	3520
	GGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC GCAGTCCACTTGGCCATCG**C**ACCTCCAGAACTGAGGAATGCA GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATT	3521
	CTGGAGGT**G**CGATGGCC	3522
	GGCCATCG**C**ACCTCCAG	3523
Hypercholesterolaemia Asp69Asn cGAT-AAT	TCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGC**G**ATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	3524
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCAT**C**GCACCTCCAGAACTGAGGAATG CAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGA	3525
	GGAGGTGC**G**ATGGCCAA	3526
	TTGGCCAT**C**GCACCTCC	3527
Hypercholesterolaemia Asp69Gly GAT-GGT	CCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCATT CCTCAGTTCTGGAGGTGCG**A**TGGCCAAGTGGACTGCGACAA CGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGC	3528
	GCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTT GTCGCAGTCCACTTGGCCA**T**CGCACCTCCAGAACTGAGGAAT GCAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGG	3529
	GAGGTGCG**A**TGGCCAAG	3530
	CTTGGCCA**T**CGCACCTC	3531
Hypercholesterolaemia Asp69Tyr cGAT-TAT	TCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGC**G**ATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG	3532

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCAT**C**GCACCTCCAGAACTGAGGAATG CAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGA	3533
	GGAGGTGC**G**ATGGCCAA	3534
	TTGGCCAT**C**GCACCTCC	3535
Hypercholesterolaemia Gln71Glu cCAA-GAA	GACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCATTCCTCA GTTCTGGAGGTGCGATGGC**C**AAGTGGACTGCGACAACGGCT CAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGCCTTTG	3536
	CAAAGGCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAG CCGTTGTCGCAGTCCACTT**G**GCCATCGCACCTCCAGAACTGA GGAATGCAGCGGTTGACACGGCCCCCACAGCTGAAGTC	3537
	GCGATGGC**C**AAGTGGAC	3538
	GTCCACTT**G**GCCATCGC	3539
Hypercholesterolaemia Cys74Gly cTGC-GGC	TGTGGGGGCCGTGTCAACCGCTGCATTCCTCAGTTCTGGAG GTGCGATGGCCAAGTGGAC**T**GCGACAACGGCTCAGACGAGC AAGGCTGTCGTAAGTGTGGCCCTGCCTTTGCTATTGAGC	3540
	GCTCAATAGCAAAGGCAGGGCCACACTTACGACAGCCTTGCT CGTCTGAGCCGTTGTCGC**A**GTCCACTTGGCCATCGCACCTC CAGAACTGAGGAATGCAGCGGTTGACACGGCCCCCACA	3541
	AAGTGGAC**T**GCGACAAC	3542
	GTTGTCGC**A**GTCCACTT	3543
Hypercholesterolaemia Ser78Term TCA-TGA	TCAACCGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAG TGGACTGCGACAACGGCT**C**AGACGAGCAAGGCTGTCGTAAG TGTGGCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCT	3544
	AGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCACACTTA CGACAGCCTTGCTCGTCT**G**AGCCGTTGTCGCAGTCCACTTGG CCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGA	3545
	CAACGGCT**C**AGACGAGC	3546
	GCTCGTCT**G**AGCCGTTG	3547
Hypercholesterolaemia Glu80Lys cGAG-AAG	CGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGA CTGCGACAACGGCTCAGAC**G**AGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3548
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCT**C**GTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3549
	GCTCAGAC**G**AGCAAGGC	3550
	GCCTTGCT**C**GTCTGAGC	3551
Hypercholesterolaemia Glu80Term cGAG-TAG	CGCTGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGA CTGCGACAACGGCTCAGAC**G**AGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA	3552
	TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCT**C**GTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG	3553
	GCTCAGAC**G**AGCAAGGC	3554

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCCTTGCT**C**GTCTGAGC	3555
Hypercholesterolaemia Gln81Term gCAA-TAA	TGCATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGC GACAACGGCTCAGACGAG**C**AAGGCTGTCGTAAGTGTGGCCC TGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGAGTG	3556
	CACTCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGG CCACACTTACGACAGCCTT**G**CTCGTCTGAGCCGTTGTCGCAG TCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA	3557
	CAGACGAG**C**AAGGCTGT	3558
	ACAGCCTT**G**CTCGTCTG	3559
Hypercholesterolaemia Cys88Arg gTGC-CGC	TGGGAGACTTCACACGGTGATGGTGGTCTCGGCCCATCCAT CCCTGCAGCCCCCAAGACG**T**GCTCCCAGGACGAGTTTCGCT GCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTG	3560
	CACAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAG CGAAACTCGTCCTGGGAGC**A**CGTCTTGGGGGCTGCAGGGAT GGATGGGCCGAGACCACCATCACCGTGTGAAGTCTCCCA	3561
	CCAAGACG**T**GCTCCCAG	3562
	CTGGGAGC**A**CGTCTTGG	3563
Hypercholesterolaemia Glu92Term cGAG-TAG	CACGGTGATGGTGGTCTCGGCCCATCCATCCCTGCAGCCCC CAAGACGTGCTCCCAGGAC**G**AGTTTCGCTGCCACGATGGGA AGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGG	3564
	CCCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTTC CCATCGTGGCAGCGAAACT**C**GTCCTGGGAGCACGTCTTGGG GGCTGCAGGGATGGATGGGCCGAGACCACCATCACCGTG	3565
	CCCAGGAC**G**AGTTTCGC	3566
	GCGAAACT**C**GTCCTGGG	3567
Hypercholesterolaemia Cys95Arg cTGC-CGC	GGTGGTCTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTG CTCCCAGGACGAGTTTCGC**T**GCCACGATGGGAAGTGCATCT CTCGGCAGTTCGTCTGTGACTCAGACCGGGACTGCTTGG	3568
	CCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGAGAG ATGCACTTCCCATCGTGGC**A**GCGAAACTCGTCCTGGGAGCA CGTCTTGGGGGCTGCAGGGATGGATGGGCCGAGACCACC	3569
	AGTTTCGC**T**GCCACGAT	3570
	ATCGTGGC**A**GCGAAACT	3571
Hypercholesterolaemia Asp97Tyr cGAT-TAT	CTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTGCTCCCA GGACGAGTTTCGCTGCCAC**G**ATGGGAAGTGCATCTCTCGGC AGTTCGTCTGTGACTCAGACCGGGACTGCTTGGACGGCT	3572
	AGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGC CGAGAGATGCACTTCCCAT**C**GTGGCAGCGAAACTCGTCCTG GGAGCACGTCTTGGGGGCTGCAGGGATGGATGGGCCGAG	3573
	GCTGCCAC**G**ATGGGAAG	3574
	CTTCCCAT**C**GTGGCAGC	3575
Hypercholesterolaemia Trp(-12)Arg cTGG-AGG	GGGTCGGGACACTGCCTGGCAGAGGCTGCGAGCATGGGGC CCTGGGGCTGGAAATTGCGC**T**GGACCGTCGCCTTGCTCCTC GCCGCGGCGGGGACTGCAGGTAAGGCTTGCTCCAGGCGCC	3576

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGCGCCTGGAGCAAGCCTTACCTGCAGTCCCCGCCGCGGC GAGGAGCAAGGCGACGGTCC**A**GCGCAATTTCCAGCCCCAGG GCCCCATGCTCGCAGCCTCTGCCAGGCAGTGTCCCGACCC	3577
	AATTGCGC**T**GGACCGTC	3578
	GACGGTCC**A**GCGCAATT	3579
Hypercholesterolaemia Trp(-18)Term TGGg-TGA	CAGCAGGTCGTGATCCGGGTCGGGACACTGCCTGGCAGAGG CTGCGAGCATGGGGCCCTG**G**GGCTGGAAATTGCGCTGGACC GTCGCCTTGCTCCTCGCCGCGGCGGGGACTGCAGGTAAG	3580
	CTTACCTGCAGTCCCCGCCGCGGCGAGGAGCAAGGCGACG GTCCAGCGCAATTTCCAGCC**C**CAGGGCCCCATGCTCGCAGC CTCTGCCAGGCAGTGTCCCGACCCGGATCACGACCTGCTG	3581
	GGGCCCTG**G**GGCTGGAA	3582
	TTCCAGCC**C**CAGGGCCC	3583
Hypercholesterolaemia Met(-21)Leu cATG-TTG	CAGCTAGGACACAGCAGGTCGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGC**A**TGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA	3584
	TCCCCGCCGCGGCGAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCA**T**GCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3585
	CTGCGAGC**A**TGGGGCCC	3586
	GGGCCCCA**T**GCTCGCAG	3587
Hypercholesterolaemia Met(-21)Val cATG-GTG	CAGCTAGGACACAGCAGGTCGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGC**A**TGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA	3588
	TCCCCGCCGCGGCGAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCA**T**GCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG	3589
	CTGCGAGC**A**TGGGGCCC	3590
	GGGCCCCA**T**GCTCGCAG	3591
Hypercholesterolaemia Ile101Phe cATC-TTC	ATCCCTGCAGCCCCCAAGACGTGCTCCCAGGACGAGTTTCG CTGCCACGATGGGAAGTGC**A**TCTCTCGGCAGTTCGTCTGTGA CTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGCCT	3592
	AGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA CAGACGAACTGCCGAGAGA**T**GCACTTCCCATCGTGGCAGCG AAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT	3593
	GGAAGTGC**A**TCTCTCGG	3594
	CCGAGAGA**T**GCACTTCC	3595
Hypercholesterolaemia Gln104Term gCAG-TAG	GCCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTGCCACGA TGGGAAGTGCATCTCTCGG**C**AGTTCGTCTGTGACTCAGACCG GGACTGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGG	3596
	CCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTCCCG GTCTGAGTCACAGACGAACT**G**CCGAGAGATGCACTTCCCATC GTGGCAGCGAAACTCGTCCTGGGAGCACGTCTTGGGGGC	3597
	TCTCTCGG**C**AGTTCGTC	3598

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GACGAACTGCCGAGAGA	3599
Hypercholesterolaemia Cys113Arg cTGC-CGC	TTTCGCTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTC TGTGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGC CTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCC	3600
	GGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGC CTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGA CGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCGAAA	3601
	ACCGGGACTGCTTGGAC	3602
	GTCCAAGCAGTCCCGGT	3603
Hypercholesterolaemia Glu119Lys cGAG-AAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	3604
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	3605
	GCTCAGACGAGGCCTCC	3606
	GGAGGCCTCGTCTGAGC	3607
Hypercholesterolaemia Glu119Term cGAG-TAG	AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT	3608
	AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT	3609
	GCTCAGACGAGGCCTCC	3610
	GGAGGCCTCGTCTGAGC	3611
Hypercholesterolaemia Cys122Term TGCc-TGA	TCGGCAGTTCGTCTGTGACTCAGACCGGGACTGCTTGGACG GCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCC GCCAGCTTCCAGTGCAACAGCTCCACCTGCATCCCCCAG	3612
	CTGGGGGATGCAGGTGGAGCTGTTGCACTGGAAGCTGGCGG GACCACAGGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCC GTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGA	3613
	GCCTCCTGCCCGGTGCT	3614
	AGCACCGGGCAGGAGGC	3615
Hypercholesterolaemia Cys127Trp TGTg-TGG	TGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGCCT CCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCCAGTGC AACAGCTCCACCTGCATCCCCCAGCTGTGGGCCTGCGAC	3616
	GTCGCAGGCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGC ACTGGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGA GGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA	3617
	CTCACCTGTGGTCCCGC	3618
	GCGGGACCACAGGTGAG	3619
Hypercholesterolaemia Gln133Term cCAG-TAG	TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT CCCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCG	3620

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CGCAGTCGGGGTCGTTGTCGCAGGCCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACT**G**GAAGCTGGCGGGACCACAGG TGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCA	3621
	CCAGCTTC**C**AGTGCAAC	3622
	GTTGCACT**G**GAAGCTGG	3623
Hypercholesterolaemia Cys134Gly gTGC-GGC	TTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTG TGGTCCCGCCAGCTTCCAG**T**GCAACAGCTCCACCTGCATCC CCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG	3624
	CTTCGCAGTCGGGGTCGTTGTCGCAGGCCCACAGCTGGGGG ATGCAGGTGGAGCTGTTGC**A**CTGGAAGCTGGCGGGACCACA GGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAA	3625
	GCTTCCAG**T**GCAACAGC	3626
	GCTGTTGC**A**CTGGAAGC	3627
Hypercholesterolaemia Cys139Gly cTGC-GGC	GAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTT CCAGTGCAACAGCTCCACC**T**GCATCCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT	3628
	ACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGC**A**GGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCTC	3629
	GCTCCACC**T**GCATCCCC	3630
	GGGGATGC**A**GGTGGAGC	3631
Hypercholesterolaemia Cys139Tyr TGC-TAC	AGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTC CAGTGCAACAGCTCCACCT**G**CATCCCCCAGCTGTGGGCCTG CGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGTG	3632
	CACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCA GGCCCACAGCTGGGGGATG**C**AGGTGGAGCTGTTGCACTGGA AGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCT	3633
	CTCCACCT**G**CATCCCCC	3634
	GGGGGATG**C**AGGTGGAG	3635
Hypercholesterolaemia Cys146Term TGCg-TGA	CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT CCCCCAGCTGTGGGCCTG**C**GACAACGACCCCGACTGCGAAG ATGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTT	3636
	AAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTTC GCAGTCGGGGTCGTTGTC**G**CAGGCCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAG	3637
	TGGGCCTG**C**GACAACGA	3638
	TCGTTGTC**G**CAGGCCCA	3639
Hypercholesterolaemia Asp147Asn cGAC-AAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGC**G**ACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3640
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGT**C**GCAGGCCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3641
	GGGCCTGC**G**ACAACGAC	3642

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GTCGTTGT**C**GCAGGCCC	3643
Hypercholesterolaemia Asp147His cGAC-CAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGC**G**ACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3644
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGT**C**GCAGGCCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3645
	GGGCCTGC**G**ACAACGAC	3646
	GTCGTTGT**C**GCAGGCCC	3647
Hypercholesterolaemia Asp147Tyr cGAC-TAC	TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGC**G**ACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT	3648
	AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGT**C**GCAGGCCCACAGCTGGGGGAT GCAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA	3649
	GGGCCTGC**G**ACAACGAC	3650
	GTCGTTGT**C**GCAGGCCC	3651
Hypercholesterolaemia Cys152Arg cTGC-CGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCCAGCTGTGGGC CTGCGACAACGACCCCGAC**T**GCGAAGATGGCTCGGATGAGT GGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3652
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC**A**GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA	3653
	ACCCCGAC**T**GCGAAGAT	3654
	ATCTTCGC**A**GTCGGGGT	3655
Hypercholesterolaemia Cys152Gly cTGC-GGC	TTCCAGTGCAACAGCTCCACCTGCATCCCCCAGCTGTGGGC CTGCGACAACGACCCCGAC**T**GCGAAGATGGCTCGGATGAGT GGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG	3656
	CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC**A**GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA	3657
	ACCCCGAC**T**GCGAAGAT	3658
	ATCTTCGC**A**GTCGGGGT	3659
Hypercholesterolaemia Cys152Trp TGCg-TGG	CCAGTGCAACAGCTCCACCTGCATCCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTG**C**GAAGATGGCTCGGATGAGTGG CCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGAC	3660
	GTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCC ACTCATCCGAGCCATCTTC**G**CAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGG	3661
	CCCGACTG**C**GAAGATGG	3662
	CCATCTTC**G**CAGTCGGG	3663
Hypercholesterolaemia Asp154Asn aGAT-AAT	TGCAACAGCTCCACCTGCATCCCCCAGCTGTGGGCCTGCGA CAACGACCCCGACTGCGAA**G**ATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGACAGTA	3664

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TACTGTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCAT**C**TTCGCAGTCGGGGTCGTTGTCG CAGGCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCA	3665
	ACTGCGAA**G**ATGGCTCG	3666
	CGAGCCAT**C**TTCGCAGT	3667
Hypercholesterolaemia Ser156Leu TCG-TTG	GCTCCACCTGCATCCCCCAGCTGTGGGCCTGCGACAACGAC CCCGACTGCGAAGATGGCT**C**GGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGCCCCTG	3668
	CAGGGGCTACTGTCCCCTTGGAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCC**G**AGCCATCTTCGCAGTCGGGGTC GTTGTCGCAGGCCCACAGCTGGGGGATGCAGGTGGAGC	3669
	AGATGGCT**C**GGATGAGT	3670
	ACTCATCC**G**AGCCATCT	3671
Hypercholesterolaemia Cys163Tyr TGT-TAT	TGTGGGCCTGCGACAACGACCCCGACTGCGAAGATGGCTCG GATGAGTGGCCGCAGCGCT**G**TAGGGGTCTTTACGTGTTCCAA GGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG	3672
	CAGTGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTTG GAACACGTAAAGACCCCTA**C**AGCGCTGCGGCCACTCATCCG AGCCATCTTCGCAGTCGGGGTCGTTGTCGCAGGCCCACA	3673
	GCAGCGCT**G**TAGGGGTC	3674
	GACCCCTA**C**AGCGCTGC	3675
Hypercholesterolaemia Tyr167Term TACg-TAG	CAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTA**C**GTGTTCCAAGGGGACAGTAGC CCCTGCTCGGCCTTCGAGTTCCACTGCCTAAGTGGCGAG	3676
	CTCGCCACTTAGGCAGTGGAACTCGAAGGCCGAGCAGGGGC TACTGTCCCCTTGGAACAC**G**TAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTG	3677
	GGTCTTTA**C**GTGTTCCA	3678
	TGGAACAC**G**TAAAGACC	3679
Hypercholesterolaemia Gln170Term cCAA-TAA	CCCGACTGCGAAGATGGCTCGGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTTC**C**AAGGGGACAGTAGCCCCTGCTC GGCCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCC	3680
	GGATGCACTCGCCACTTAGGCAGTGGAACTCGAAGGCCGAG CAGGGGCTACTGTCCCCTT**G**GAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCCGAGCCATCTTCGCAGTCGGG	3681
	ACGTGTTC**C**AAGGGGAC	3682
	GTCCCCTT**G**GAACACGT	3683
Hypercholesterolaemia Cys176Phe TGC-TTC	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTC CAAGGGGACAGTAGCCCCT**G**CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3684
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAACTCGAAGGCCGAG**C**AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3685
	TAGCCCCT**G**CTCGGCCT	3686

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCCGAG**C**AGGGGCTA	3687
Hypercholesterolaemia Cys176Tyr TGC-TAC	CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTC CAAGGGGACAGTAGCCCCT**G**CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA	3688
	TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAACTCGAAGGCCGAG**C**AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG	3689
	TAGCCCCT**G**CTCGGCCT	3690
	AGGCCGAG**C**AGGGGCTA	3691
Hypercholesterolaemia Ser177Leu TCG-TTG	ATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAG GGGACAGTAGCCCCTGCT**C**GGCCTTCGAGTTCCACTGCCTA AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGG	3692
	CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAG GCAGTGGAACTCGAAGGCC**G**AGCAGGGGCTACTGTCCCCTT GGAACACGTAAAGACCCCTACAGCGCTGCGGCCACTCAT	3693
	CCCCTGCT**C**GGCCTTCG	3694
	CGAAGGCC**G**AGCAGGGG	3695
Hypercholesterolaemia Glu187Lys cGAG-AAG	TACGTGTTCCAAGGGGACAGTAGCCCCTGCTCGGCCTTCGA GTTCCACTGCCTAAGTGGC**G**AGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG	3696
	CGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGC CAGCTGGAGTGGATGCACT**C**GCCACTTAGGCAGTGGAACTC GAAGGCCGAGCAGGGGCTACTGTCCCCTTGGAACACGTA	3697
	TAAGTGGC**G**AGTGCATC	3698
	GATGCACT**C**GCCACTTA	3699
Hypercholesterolaemia His190Tyr cCAC-TAC	CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATC**C**ACTCCAGCTGGCGCTGTGATG GTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACT	3700
	AGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCAT CACAGCGCCAGCTGGAGT**G**GATGCACTCGCCACTTAGGCAG TGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTTG	3701
	AGTGCATC**C**ACTCCAGC	3702
	GCTGGAGT**G**GATGCACT	3703
Hypercholesterolaemia Gly198Asp GGC-GAC	CCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCA GCTGGCGCTGTGATGGTG**G**CCCCGACTGCAAGGACAAATCT GACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGG	3704
	CCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGAT TTGTCCTTGCAGTCGGGG**C**CACCATCACAGCGCCAGCTGGA GTGGATGCACTCGCCACTTAGGCAGTGGAACTCGAAGG	3705
	TGATGGTG**G**CCCCGACT	3706
	AGTCGGGG**C**CACCATCA	3707
Hypercholesterolaemia Asp200Asn cGAC-AAC	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTG GCGCTGTGATGGTGGCCCC**G**ACTGCAAGGACAAATCTGACG AGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3708

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCG TCAGATTTGTCCTTGCAGT**C**GGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTC	3709
	GTGGCCCC**G**ACTGCAAG	3710
	CTTGCAGT**C**GGGGCCAC	3711
Hypercholesterolaemia Asp200Gly GAC-GGC	AGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCG**A**CTGCAAGGACAAATCTGACGAG GAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGG	3712
	CCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTC GTCAGATTTGTCCTTGCAG**T**CGGGGCCACCATCACAGCGCCA GCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACT	3713
	TGGCCCCG**A**CTGCAAGG	3714
	CCTTGCAG**T**CGGGGCCA	3715
Hypercholesterolaemia Asp200Tyr cGAC-TAC	GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTG GCGCTGTGATGGTGGCCCC**G**ACTGCAAGGACAAATCTGACG AGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG	3716
	CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCG TCAGATTTGTCCTTGCAGT**C**GGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTC	3717
	GTGGCCCC**G**ACTGCAAG	3718
	CTTGCAGT**C**GGGGCCAC	3719
Hypercholesterolaemia Cys201Term TGCa-TGA	CCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTG**C**AAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGT	3720
	ACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTT CCTCGTCAGATTTGTCCTT**G**CAGTCGGGGCCACCATCACAGC GCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGG	3721
	CCCGACTG**C**AAGGACAA	3722
	TTGTCCTT**G**CAGTCGGG	3723
Hypercholesterolaemia Cys201Tyr TGC-TAC	TCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGC TGTGATGGTGGCCCCGACT**G**CAAGGACAAATCTGACGAGGA AAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCG	3724
	CGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTC CTCGTCAGATTTGTCCTTG**C**AGTCGGGGCCACCATCACAGCG CCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGA	3725
	CCCCGACT**G**CAAGGACA	3726
	TGTCCTTG**C**AGTCGGGG	3727
Hypercholesterolaemia Asp203Asn gGAC-AAC	TGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA TGGTGGCCCCGACTGCAAG**G**ACAAATCTGACGAGGAAAACT GCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTA	3728
	TAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCCTCGTCAGATTTGT**C**CTTGCAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA	3729
	ACTGCAAG**G**ACAAATCT	3730

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGATTTGTCCTTGCAGT	3731
Hypercholesterolaemia Asp203Gly GAC-GGC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3732
	ATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3733
	CTGCAAGGACAAATCTG	3734
	CAGATTTGTCCTTGCAG	3735
Hypercholesterolaemia Asp203Val GAC-GTC	GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT	3736
	ATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC	3737
	CTGCAAGGACAAATCTG	3738
	CAGATTTGTCCTTGCAG	3739
Hypercholesterolaemia Ser205Pro aTCT-CCT	AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCT	3740
	AGGTGATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACT	3741
	AGGACAAATCTGACGAG	3742
	CTCGTCAGATTTGTCCT	3743
Hypercholesterolaemia Asp206Glu GACg-GAG	CGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCC	3744
	GGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCG	3745
	AAATCTGACGAGGAAAA	3746
	TTTTCCTCGTCAGATTT	3747
Hypercholesterolaemia Glu207Gln cGAG-CAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3748
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3749
	AATCTGACGAGGAAAAC	3750
	GTTTTCCTCGTCAGATT	3751

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Hypercholesterolaemia Glu207Lys cGAG-AAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC**G**AGGAAAACTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3752
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCCT**C**GTCAGATTTGTCCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3753
	AATCTGAC**G**AGGAAAAC	3754
	GTTTTCCT**C**GTCAGATT	3755
Hypercholesterolaemia Glu207Term cGAG-TAG	GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC**G**AGGAAAACTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT	3756
	AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCCT**C**GTCAGATTTGTCCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC	3757
	AATCTGAC**G**AGGAAAAC	3758
	GTTTTCCT**C**GTCAGATT	3759
Hypercholesterolaemia Glu219Lys cGAA-AAA	TCTTGAGAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGG CCACCTGTCGCCCTGAC**G**AATTCCAGTGCTCTGATGGAAACT GCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG	3760
	CATATTCCCGGTCACACTGCCGGCTGCCATGGATGCAGTTTC CATCAGAGCACTGGAATT**C**GTCAGGGCGACAGGTGGCCACA GCTGGAAAACAGGACAGAGTGTGTTGATTTTCTCAAGA	3761
	GCCCTGAC**G**AATTCCAG	3762
	CTGGAATT**C**GTCAGGGC	3763
Hypercholesterolaemia Gln221Term cCAG-TAG	GAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGGCCACCT GTCGCCCTGACGAATTC**C**AGTGCTCTGATGGAAACTGCATCC ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCA	3764
	TGCAGTCATATTCCCGGTCACACTGCCGGCTGCCATGGATGC AGTTTCCATCAGAGCACT**G**GAATTCGTCAGGGCGACAGGTGG CCACAGCTGGAAAACAGGACAGAGTGTGTTGATTTTC	3765
	ACGAATTC**C**AGTGCTCT	3766
	AGAGCACT**G**GAATTCGT	3767
Hypercholesterolaemia Cys227Phe TGC-TTC	CCTGTTTTCCAGCTGTGGCCACCTGTCGCCCTGACGAATTCC AGTGCTCTGATGGAAACT**G**CATCCATGGCAGCCGGCAGTGT GACCGGGAATATGACTGCAAGGACATGAGCGATGAAGT	3768
	ACTTCATCGCTCATGTCCTTGCAGTCATATTCCCGGTCACACT GCCGGCTGCCATGGATG**C**AGTTTCCATCAGAGCACTGGAATT CGTCAGGGCGACAGGTGGCCACAGCTGGAAAACAGG	3769
	TGGAAACT**G**CATCCATG	3770
	CATGGATG**C**AGTTTCCA	3771
Hypercholesterolaemia Asp235Glu GACc-GAA	TCGCCCTGACGAATTCCAGTGCTCTGATGGAAACTGCATCCA TGGCAGCCGGCAGTGTGA**C**CGGGAATATGACTGCAAGGACA TGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGG	3772

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAGCGCTCACCATTAACGCAGCCAACTTCATCGCTCATGTC CTTGCAGTCATATTCCCG**G**TCACACTGCCGGCTGCCATGGAT GCAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGA	3773
	CAGTGTGA**C**CGGGAATA	3774
	TATTCCCG**G**TCACACTG	3775
Hypercholesterolaemia Asp235Gly GAC-GGC	GTCGCCCTGACGAATTCCAGTGCTCTGATGGAAACTGCATCC ATGGCAGCCGGCAGTGTG**A**CCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTG	3776
	CAGCGCTCACCATTAACGCAGCCAACTTCATCGCTCATGTCC TTGCAGTCATATTCCCGG**T**CACACTGCCGGCTGCCATGGATG CAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGAC	3777
	GCAGTGTG**A**CCGGGAAT	3778
	ATTCCCGG**T**CACACTGC	3779
Hypercholesterolaemia Glu237Lys gGAA-AAA	CCTGACGAATTCCAGTGCTCTGATGGAAACTGCATCCATGGC AGCCGGCAGTGTGACCGG**G**AATATGACTGCAAGGACATGAG CGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGGCCAT	3780
	ATGGCCAGCGCTCACCATTAACGCAGCCAACTTCATCGCTCA TGTCCTTGCAGTCATATT**C**CCGGTCACACTGCCGGCTGCCAT GGATGCAGTTTCCATCAGAGCACTGGAATTCGTCAGG	3781
	GTGACCGG**G**AATATGAC	3782
	GTCATATT**C**CCGGTCAC	3783
Hypercholesterolaemia Cys240Phe TGC-TTC	TCCAGTGCTCTGATGGAAACTGCATCCATGGCAGCCGGCAGT GTGACCGGGAATATGACT**G**CAAGGACATGAGCGATGAAGTTG GCTGCGTTAATGGTGAGCGCTGGCCATCTGGTTTTCC	3784
	GGAAAACCAGATGGCCAGCGCTCACCATTAACGCAGCCAACT TCATCGCTCATGTCCTTG**C**AGTCATATTCCCGGTCACACTGC CGGCTGCCATGGATGCAGTTTCCATCAGAGCACTGGA	3785
	ATATGACT**G**CAAGGACA	3786
	TGTCCTTG**C**AGTCATAT	3787
Hypercholesterolaemia Asp245Glu GATg-GAA	AAACTGCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG ACTGCAAGGACATGAGCGA**T**GAAGTTGGCTGCGTTAATGGTG AGCGCTGGCCATCTGGTTTTCCATCCCCCATTCTCTGT	3788
	ACAGAGAATGGGGGATGGAAAACCAGATGGCCAGCGCTCAC CATTAACGCAGCCAACTTC**A**TCGCTCATGTCCTTGCAGTCATA TTCCCGGTCACACTGCCGGCTGCCATGGATGCAGTTT	3789
	ATGAGCGA**T**GAAGTTGG	3790
	CCAACTTC**A**TCGCTCAT	3791
Hypercholesterolaemia Cys249Tyr TGC-TAC	ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCT**G**CGTTAATGGTGAGCGCTGGCC ATCTGGTTTTCCATCCCCCATTCTCTGTGCCTTGCTGCT	3792
	AGCAGCAAGGCACAGAGAATGGGGGATGGAAAACCAGATGG CCAGCGCTCACCATTAACG**C**AGCCAACTTCATCGCTCATGTC CTTGCAGTCATATTCCCGGTCACACTGCCGGCTGCCAT	3793
	AGTTGGCT**G**CGTTAATG	3794

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
-	CATTAACG**C**AGCCAACT	3795
Hypercholesterolaemia Glu256Lys cGAG-AAG	AGGCTCAGACACACCTGACCTTCCTCCTTCCTCTCTCTGGCT CTCACAGTGACACTCTGC**G**AGGGACCCAACAAGTTCAAGTGT CACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCA	3796
	TGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACACT TGAACTTGTTGGGTCCCT**C**GCAGAGTGTCACTGTGAGAGCCA GAGAGAGGAAGGAGGAAGGTCAGGTGTGTCTGAGCCT	3797
	CACTCTGC**G**AGGGACCC	3798
	GGGTCCCT**C**GCAGAGTG	3799
Hypercholesterolaemia Ser265Arg AGCg-AGA	CCTCTCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAA CAAGTTCAAGTGTCACAG**C**GGCGAATGCATCACCCTGGACAA AGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCA	3800
	TGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTC CAGGGTGATGCATTCGCC**G**CTGTGACACTTGAACTTGTTGGG TCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGAGAGG	3801
	TGTCACAG**C**GGCGAATG	3802
	CATTCGCC**G**CTGTGACA	3803
Hypercholesterolaemia Glu267Lys cGAA-AAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTCACAGCGGC**G**AATGCATCACCCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3804
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGATGCATT**C**GCCGCTGTGACACTTGAACTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3805
	ACAGCGGC**G**AATGCATC	3806
	GATGCATT**C**GCCGCTGT	3807
Hypercholesterolaemia Glu267Term cGAA-TAA	TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTCACAGCGGC**G**AATGCATCACCCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG	3808
	CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGATGCATT**C**GCCGCTGTGACACTTGAACTTGT TGGGTCCCTCGCAGAGTGTCACTGTGAGAGCCAGAGA	3809
	ACAGCGGC**G**AATGCATC	3810
	GATGCATT**C**GCCGCTGT	3811
Hypercholesterolaemia Lys273Glu cAAA-GAA	ACACTCTGCGAGGGACCCAACAAGTTCAAGTGTCACAGCGG CGAATGCATCACCCTGGAC**A**AAGTCTGCAACATGGCTAGAGA CTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCG	3812
	CGCACTCTTTGATGGGTTCATCTGACCAGTCCCGGCAGTCTC TAGCCATGTTGCAGACTT**T**GTCCAGGGTGATGCATTCGCCGC TGTGACACTTGAACTTGTTGGGTCCCTCGCAGAGTGT	3813
	CCCTGGAC**A**AAGTCTGC	3814
	GCAGACTT**T**GTCCAGGG	3815
Hypercholesterolaemia Cys275Term TGCa-TGA	CGAGGGACCCAACAAGTTCAAGTGTCACAGCGGCGAATGCA TCACCCTGGACAAAGTCTG**C**AACATGGCTAGAGACTGCCGG GACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCT	3816

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGTCCCGGCAGTCTCTAGCCATGTT**G**CAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACACTTGAACTTGTTGGGTCCCTCG	3817
	AAAGTCTG**C**AACATGGC	3818
	GCCATGTT**G**CAGACTTT	3819
Hypercholesterolaemia Asp280Gly GAC-GGC	AGTTCAAGTGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAG**A**CTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCT	3820
	AGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGTCCCGGCAG**T**CTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACACTTGAACT	3821
	GGCTAGAG**A**CTGCCGGG	3822
	CCCGGCAG**T**CTCTAGCC	3823
Hypercholesterolaemia Cys281Tyr TGC-TAC	TCAAGTGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACT**G**CCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGC	3824
	GCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGTCCCGG**C**AGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACACTTGA	3825
	TAGAGACT**G**CCGGGACT	3826
	AGTCCCGG**C**AGTCTCTA	3827
Hypercholesterolaemia Asp283Asn gGAC-AAC	TGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGG**G**ACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3828
	ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGT**C**CCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA	3829
	ACTGCCGG**G**ACTGGTCA	3830
	TGACCAGT**C**CCGGCAGT	3831
Hypercholesterolaemia Asp283Glu GACt-GAG	TCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGA**C**TGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTT	3832
	AAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCA**G**TCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGA	3833
	TGCCGGGA**C**TGGTCAGA	3834
	TCTGACCA**G**TCCCGGCA	3835
Hypercholesterolaemia Asp283Tyr gGAC-TAC	TGTCACAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGG**G**ACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT	3836
	ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGACCAGT**C**CCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA	3837
	ACTGCCGG**G**ACTGGTCA	3838

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGACCAGT**C**CCGGCAGT	3839
Hypercholesterolaemia Trp284Term TGGt-TGA	CAGCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTG**G**TCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTG	3840
	CACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCTGA**C**CAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGCTG	3841
	CGGGACTG**G**TCAGATGA	3842
	TCATCTGA**C**CAGTCCCG	3843
Hypercholesterolaemia Ser285Leu TCA-TTA	GCGGCGAATGCATCACCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGT**C**AGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGG	3844
	CCCACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCATCT**G**ACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTCGCCGC	3845
	GGACTGGT**C**AGATGAAC	3846
	GTTCATCT**G**ACCAGTCC	3847
Hypercholesterolaemia Lys290Arg AAA-AGA	CCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCA**A**AGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGGGAGCCAGGAAAGGGA	3848
	TCCCTTTCCTGGCTCCCCACAAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCT**T**TGATGGGTTCATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGG	3849
	ACCCATCA**A**AGAGTGCG	3850
	CGCACTCT**T**TGATGGGT	3851
Hypercholesterolaemia Cys297Phe TGC-TTC	GGGTAGGGGCCCGAGAGTGACCAGTCTGCATCCCCTGGCCCTGCGCAGGGACCAACGAAT**G**CTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3852
	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAG**C**ATTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCTACCC	3853
	CAACGAAT**G**CTTGGACA	3854
	TGTCCAAG**C**ATTCGTTG	3855
Hypercholesterolaemia Cys297Tyr TGC-TAC	GGGTAGGGGCCCGAGAGTGACCAGTCTGCATCCCCTGGCCCTGCGCAGGGACCAACGAAT**G**CTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG	3856
	CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAG**C**ATTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCTACCC	3857
	CAACGAAT**G**CTTGGACA	3858
	TGTCCAAG**C**ATTCGTTG	3859
Hypercholesterolaemia His306Tyr cCAC-TAC	TGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCC**C**ACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGG	3860

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGT**G**GGAACAGCCGCCGTTGTTGTCCAAGCATTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCA	3861
	GCTGTTCC**C**ACGTCTGC	3862
	GCAGACGT**G**GGAACAGC	3863
Hypercholesterolaemia Cys308Gly cTGC-GGC	CCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCCACGTC**T**GCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCC	3864
	GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGC**A**GACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCGTTGGTCCCTGCGCAGGGCCAGGG	3865
	CCCACGTC**T**GCAATGAC	3866
	GTCATTGC**A**GACGTGGG	3867
Hypercholesterolaemia Cys308Tyr TGC-TAC	CCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCCACGTCT**G**CAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCA	3868
	TGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTG**C**AGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCGTTGGTCCCTGCGCAGGGCCAGG	3869
	CCACGTCT**G**CAATGACC	3870
	GGTCATTG**C**AGACGTGG	3871
Hypercholesterolaemia Gly314Ser cGGC-AGC	ACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATC**G**GCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTG	3872
	CACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGC**C**GATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCGTTGGT	3873
	TTAAGATC**G**GCTACGAG	3874
	CTCGTAGC**C**GATCTTAA	3875
Hypercholesterolaemia Gly314Val GGC-GTC	CCAACGAATGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCG**G**CTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGA	3876
	TCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAG**C**CGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCGTTGG	3877
	TAAGATCG**G**CTACGAGT	3878
	ACTCGTAG**C**CGATCTTA	3879
Hypercholesterolaemia Tyr315Term TACg-TAA	CGAATGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTA**C**GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTC	3880
	GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTC**G**TAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTCG	3881
	ATCGGCTA**C**GAGTGCCT	3882

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGGCACTC**G**TAGCCGAT	3883
Hypercholesterolaemia Cys317Gly gTGC-GGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGAC CTTAAGATCGGCTACGAG**T**GCCTGTGCCCCGACGGCTTCCA GCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG	3884
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGG AAGCCGTCGGGGCACAGGC**A**CTCGTAGCCGATCTTAAGGTC ATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3885
	GCTACGAG**T**GCCTGTGC	3886
	GCACAGGC**A**CTCGTAGC	3887
Hypercholesterolaemia Cys317Ser gTGC-AGC	TGCTTGGACAACAACGGCGGCTGTTCCCACGTCTGCAATGAC CTTAAGATCGGCTACGAG**T**GCCTGTGCCCCGACGGCTTCCA GCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG	3888
	CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGG AAGCCGTCGGGGCACAGGC**A**CTCGTAGCCGATCTTAAGGTC ATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA	3889
	GCTACGAG**T**GCCTGTGC	3890
	GCACAGGC**A**CTCGTAGC	3891
Hypercholesterolaemia Pro320Arg CCC-CGC	ACAACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCG GCTACGAGTGCCTGTGCCC**C**CGACGGCTTCCAGCTGGTGGCC CAGCGAAGATGCGAAGGTGATTTCCGGGTGGACTGAG	3892
	CTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCC ACCAGCTGGAAGCCGTCG**G**GGCACAGGCACTCGTAGCCGAT CTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGT	3893
	CCTGTGCC**C**CGACGGCT	3894
	AGCCGTCG**G**GGCACAGG	3895
Hypercholesterolaemia Asp321Asn cGAC-AAC	AACGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGC TACGAGTGCCTGTGCCCC**G**ACGGCTTCCAGCTGGTGGCCCA GCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCC	3896
	GGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGG CCACCAGCTGGAAGCCGT**C**GGGGCACAGGCACTCGTAGCCG ATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTT	3897
	TGTGCCCC**G**ACGGCTTC	3898
	GAAGCCGT**C**GGGGCACA	3899
Hypercholesterolaemia Asp321Glu GACg-GAG	CGGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTA CGAGTGCCTGTGCCCCGA**C**GGCTTCCAGCTGGTGGCCCAGC GAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCT	3900
	AGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTG GGCCACCAGCTGGAAGCC**G**TCGGGGCACAGGCACTCGTAG CCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCG	3901
	TGCCCCGA**C**GGCTTCCA	3902
	TGGAAGCC**G**TCGGGGCA	3903
Hypercholesterolaemia Gly322Ser cGGC-AGC	GGCGGCTGTTCCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGAC**G**GCTTCCAGCTGGTGGCCCAGCG AAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTG	3904

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CAGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGC**C**GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCC	3905
	GCCCCGAC**G**GCTTCCAG	3906
	CTGGAAGC**C**GTCGGGGC	3907
Hypercholesterolaemia Gln324Term cCAG-TAG	TGTTCCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTC**C**AGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCC	3908
	GGGGCCCAGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCT**G**GAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACA	3909
	ACGGCTTC**C**AGCTGGTG	3910
	CACCAGCT**G**GAAGCCGT	3911
Hypercholesterolaemia Arg329Pro CGA-CCA	ATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGC**G**AAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGAC	3912
	GTCAGGAAGCGCAGAGGGGGCCCAGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTT**C**GCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCAT	3913
	GGCCCAGC**G**AAGATGCG	3914
	CGCATCTT**C**GCTGGGCC	3915
Hypercholesterolaemia Arg329Term gCGA-TGA	AATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAG**C**GAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGA	3916
	TCAGGAAGCGCAGAGGGGGCCCAGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTC**G**CTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATT	3917
	TGGCCCAG**C**GAAGATGC	3918
	GCATCTTC**G**CTGGGCCA	3919
Hypercholesterolaemia Glu336Lys tGAG-AAG	TCTAGCCATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTCTCTCTTCCAGATATCGAT**G**AGTGTCAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGT	3920
	ACTTGTAGCCACCCTCCAGGTTCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTGACACT**C**ATCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGAGGCTCTTCCCCAATGGCTAGA	3921
	ATATCGAT**G**AGTGTCAG	3922
	CTGACACT**C**ATCGATAT	3923
Hypercholesterolaemia Gln338Term tCAG-TAG	CATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTCTCTCTTCCAGATATCGATGAGTGT**C**AGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGT	3924
	ACTGGCACTTGTAGCCACCCTCCAGGTTCACGCAGAGCTGGCTGCAGGTGTCGGGATCCT**G**ACACTCATCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGAGGCTCTTCCCCAATG	3925
	ATGAGTGT**C**AGGATCCC	3926

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
-	GGGATCCTGACACTCAT	3927
Hypercholesterolaemia Cys343Arg cTGC-CGC	TCCCCACCAAGCCTCTTTCTCTCTCTTCCAGATATCGATGAGT GTCAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTG GAGGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCC	3928
	GGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCCAGGT TCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTGACACTCA TCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGA	3929
	CCGACACCTGCAGCCAG	3930
	CTGGCTGCAGGTGTCGG	3931
Hypercholesterolaemia Gln345Arg CAG-CGG	CAAGCCTCTTTCTCTCTCTTCCAGATATCGATGAGTGTCAGGA TCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTG GCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGA	3932
	TCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCC TCCAGGTTCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG ACACTCATCGATATCTGGAAGAGAGAGAAAGAGGCTTG	3933
	CTGCAGCCAGCTCTGCG	3934
	CGCAGAGCTGGCTGCAG	3935
Hypercholesterolaemia Cys347Tyr TGC-TAC	TCTTTCTCTCTCTTCCAGATATCGATGAGTGTCAGGATCCCGA CACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACA AGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCA	3936
	TGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTA GCCACCCTCCAGGTTCACGCAGAGCTGGCTGCAGGTGTCGG GATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGA	3937
	CCAGCTCTGCGTGAACC	3938
	GGTTCACGCAGAGCTGG	3939
Hypercholesterolaemia Cys347Arg cTGC-CGC	CTCTTTCTCTCTCTTCCAGATATCGATGAGTGTCAGGATCCCG ACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTAC AAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCC	3940
	GGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTCACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGAG	3941
	GCCAGCTCTGCGTGAAC	3942
	GTTCACGCAGAGCTGGC	3943
Hypercholesterolaemia Gly352Asp GGT-GAT	CAGATATCGATGAGTGTCAGGATCCCGACACCTGCAGCCAGC TCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAG GAAGGCTTCCAGCTGGACCCCCACACGAAGGCCTGCAA	3944
	TTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTC ACACTGGCACTTGTAGCCACCCTCCAGGTTCACGCAGAGCTG GCTGCAGGTGTCGGGATCCTGACACTCATCGATATCTG	3945
	CCTGGAGGGTGGCTACA	3946
	TGTAGCCACCCTCCAGG	3947
Hypercholesterolaemia Tyr354Cys TAC-TGC	TCGATGAGTGTCAGGATCCCGACACCTGCAGCCAGCTCTGC GTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAGGAAGG CTTCCAGCTGGACCCCCACACGAAGGCCTGCAAGGCTGT	3948

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACAGCCTTGCAGGCCTTCGTGTGGGGTCCAGCTGGAAGCC TTCCTCACACTGGCACTTGTAGCCACCCTCCAGGTTCACGCA GAGCTGGCTGCAGGTGTCGGGATCCTGACACTCATCGA	3949
	GGGTGGCTACAAGTGCC	3950
	GGCACTTGTAGCCACCC	3951
Hypercholesterolaemia Cys358Arg gTGT-CGT	CAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGA GGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGG ACCCCCACACGAAGGCCTGCAAGGCTGTGGGTGAGCACG	3952
	CGTGCTCACCCACAGCCTTGCAGGCCTTCGTGTGGGGTCC AGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCC AGGTTCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG	3953
	AGTGCCAGTGTGAGGAA	3954
	TTCCTCACACTGGCACT	3955
Hypercholesterolaemia Gln363Term cCAG-TAG	TGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGTG CCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCACACGAAGG CCTGCAAGGCTGTGGGTGAGCACGGGAAGGCGGCGGGTG	3956
	CACCCGCCGCCTTCCCGTGCTCACCCACAGCCTTGCAGGCC TTCGTGTGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCA CTTGTAGCCACCCTCCAGGTTCACGCAGAGCTGGCTGCA	3957
	AAGGCTTCCAGCTGGAC	3958
	GTCCAGCTGGAAGCCTT	3959

EXAMPLE 22
UDP-glucuronosyltransferase - UGT1

Mutations in the human UGT1 gene result in a range of disease syndromes, ranging from relatively common diseases such as Gilbert's syndrome, which effects up to 7% of the population, to rare disorders such as Crigler-Najjar syndrome. Symptoms of these diseases are the result of diminished bilirubin conjugation and typically present with jaundice or, when mild, as an incidental finding during routing laboratory analysis. Severe cases of Crigler-Najjar syndrome are caused by an absence of UGT1 activity and the majority of these patients die in the neonatal period. The only known treatment is liver transplant. The attached table discloses the correcting oligonucleotide base sequences for the UGT1 oligonucleotides of the invention.

Table 29
UGT1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Crigler-Najjar syndrome 2 Leu15Arg CTG-CGG	GCAGGAGCAAAGGCGCCATGGCTGTGGAGTCCCAGGGCGG ACGCCCACTTGTCCTGGGCC**T**GCTGCTGTGTGTGCTGGGCC CAGTGGTGTCCCATGCTGGGAAGATACTGTTGATCCCAGT	3960
	ACTGGGATCAACAGTATCTTCCCAGCATGGACACCACTGGG CCCAGCACACACAGCAGC**A**GGCCCAGGACAAGTGGGCGTCC GCCCTGGGACTCCACAGCCATGGCGCCTTTGCTCCTGC	3961
	CCTGGGCC**T**GCTGCTGT	3962
	ACAGCAGC**A**GGCCCAGG	3963
Crigler-Najjar syndrome 1 Gln49Term CAG-TAG	GGGAAGATACTGTTGATCCCAGTGGATGGCAGCCACTGGCT GAGCATGCTTGGGGCCATC**C**AGCAGCTGCAGCAGAGGGGAC ATGAAATAGTTGTCCTAGCACCTGACGCCTCGTTGTACA	3964
	TGTACAACGAGGCGTCAGGTGCTAGGACAACTATTTCATGTC CCCTCTGCTGCAGCTGCT**G**GATGGCCCCAAGCATGCTCAGC CAGTGGCTGCCATCCACTGGGATCAACAGTATCTTCCC	3965
	GGGCCATC**C**AGCAGCTG	3966
	CAGCTGCT**G**GATGGCCC	3967
Crigler-Najjar syndrome 1 Gly71Arg GGA-AGA	CAGCAGAGGGGACATGAAATAGTTGTCCTAGCACCTGACGCC TCGTTGTACATCAGAGAC**G**GAGCATTTTACACCTTGAAGACGT ACCCTGTGCCATTCCAAAGGGAGGATGTGAAAGAGT	3968
	ACTCTTTCACATCCTCCCTTTGGAATGGCACAGGGTACGTCTT CAAGGTGTAAAATGCTC**C**GTCTCTGATGTACAACGAGGCGTC AGGTGCTAGGACAACTATTTCATGTCCCCTCTGCTG	3969
	TCAGAGAC**G**GAGCATTT	3970
	AAATGCTC**C**GTCTCTGA	3971
Gilbert syndrome Pro229Gln CCG-CAG	GGGTGAAGAACATGCTCATTGCCTTTTCACAGAACTTTCTGTG CGACGTGGTTTATTCCC**C**GTATGCAACCCTTGCCTCAGAATT CCTTCAGAGAGAGGTGACTGTCCAGGACCTATTGAG	3972
	CTCAATAGGTCCTGGACAGTCACCTCTCTCTGAAGGAATTCT GAGGCAAGGGTTGCATAC**G**GGGAATAAACCACGTCGCACAG AAAGTTCTGTGAAAAGGCAATGAGCATGTTCTTCACCC	3973
	TTATTCCC**C**GTATGCAA	3974
	TTGCATAC**G**GGGAATAA	3975
Crigler-Najjar syndrome 1 Cys280Term TGC-TGA	TGTGAAGGATTACCCTAGGCCCATCATGCCCAATATGGTTTTT GTTGGTGGAATCAACTG**C**CTTCACCAAAATCCACTATCCCAG GTGTGTATTGGAGTGGGACTTTTACATGCGTATATT	3976
	AATATACGCATGTAAAAGTCCCACTCCAATACACACCTGGGAT AGTGGATTTTGGTGAAG**G**CAGTTGATTCCACCAACAAAAACC ATATTGGGCATGATGGGCCTAGGGTAATCCTTCACA	3977

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATCAACTG**C**CTTCACCA	3978
	TGGTGAAG**G**CAGTTGAT	3979
Crigler-Najjar syndrome 1 Ala292Val GCC-GTC	ATCAAAGAATATGAGAAAAAATTAACTGAAAATTTTTCTTCTGG CTCTAGGAATTTGAAG**C**CTACATTAATGCTTCTGGAGAACATG GAATTGTGGTTTTCTCTTTGGGATCAATGGTCTC	3980
	GAGACCATTGATCCCAAAGAGAAAACCACAATTCCATGTTCTC CAGAAGCATTAATGTAG**G**CTTCAAATTCCTAGAGCCAGAAGAA AAATTTTTCAGTTAATTTTTTCTCATATTCTTTGAT	3981
	ATTTGAAG**C**CTACATTA	3982
	TAATGTAG**G**CTTCAAAT	3983
Crigler-Najjar syndrome 1 Gly308Glu GGA-GAA	AGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAAT TGTGGTTTTCTCTTTGG**G**ATCAATGGTCTCAGAAATTCCAGAG AAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAA	3984
	TTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAA TTTCTGAGACCATTGAT**C**CCAAAGAGAAAACCACAATTCCATG TTCTCCAGAAGCATTAATGTAGGCTTCAAATTCCT	3985
	CTCTTTGG**G**ATCAATGG	3986
	CCATTGAT**C**CCAAAGAG	3987
Crigler-Najjar syndrome 1 Gln331Term CAG-TAG	GTCTCAGAAATTCCAGAGAAGAAAGCTATGGCAATTGCTGAT GCTTTGGGCAAAATCCCT**C**AGACAGTAAGAAGATTCTATACCA TGGCCTCATATCTATTTTCACAGGAGCGCTAATCCC	3988
	GGGATTAGCGCTCCTGTGAAAATAGATATGAGGCCATGGTAT AGAATCTTCTTACTGTCT**G**AGGGATTTTGCCCAAAGCATCAGC AATTGCCATAGCTTTCTTCTCTGGAATTTCTGAGAC	3989
	AAATCCCT**C**AGACAGTA	3990
	TACTGTCT**G**AGGGATTT	3991
Crigler-Najjar syndrome 1 Trp335Term TGG-TGA	TCTAATCATATTATGTTCTTTCTTTACGTTCTGCTCTTTTTGCC CCTCCCAGGTCCTGTG**G**CGGTACACTGGAACCCGACCATCG AATCTTGCGAACAACACGATACTTGTTAAGTGGCTA	3992
	TAGCCACTTAACAAGTATCGTGTTGTTCGCAAGATTCGATGGT CGGGTTCCAGTGTACCG**C**CACAGGACCTGGGAGGGGCAAAA AGAGCAGAACGTAAAGAAAGAACATAATATGATTAGA	3993
	GTCCTGTG**G**CGGTACAC	3994
	GTGTACCG**C**CACAGGAC	3995
Crigler-Najjar syndrome 1 Gln357Arg CAA-CGA	ACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATAC TTGTTAAGTGGCTACCCC**A**AAACGATCTGCTTGGTATGTTGG GCGGATTGGATGTATAGGTCAAACCAGGGTCAAATTA	3996
	TAATTTGACCCTGGTTTGACCTATACATCCAATCCC[illegible]CCAACA TACCAAGCAGATCGTTT**T**GGGGTAGCCACTTAACAAGTATCGT GTTGTTCGCAAGATTCGATGGTCGGGTTCCAGTGT	3997

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GCTACCCC**A**AAACGATC	3998
	GATCGTTT**T**GGGGTAGC	3999
Crigler-Najjar syndrome 1 Gln357Term CAA-TAA	TACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATA CTTGTTAAGTGGCTACCC**C**AAAACGATCTGCTTGGTATGTTG GGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATT	4000
	AATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACAT ACCAAGCAGATCGTTTT**G**GGGTAGCCACTTAACAAGTATCGT GTTGTTCGCAAGATTCGATGGTCGGGTTCCAGTGTA	4001
	GGCTACCC**C**AAAACGAT	4002
	ATCGTTTT**G**GGGTAGCC	4003
Gilbert syndrome Arg367Gly CGT-GGT	AACTCAGAGATGTAACTGCTGACATCCTCCCTATTTTGCATCT CAGGTCACCCGATGACC**C**GTGCCTTTATCACCCATGCTGGTT CCCATGGTGTTTATGAAAGCATATGCAATGGCGTTC	4004
	GAACGCCATTGCATATGCTTTCATAAACACCATGGGAACCAG CATGGGTGATAAAGGCAC**G**GGTCATCGGGTGACCTGAGATG CAAAATAGGGAGGATGTCAGCAGTTACATCTCTGAGTT	4005
	CGATGACC**C**GTGCCTTT	4006
	AAAGGCAC**G**GGTCATCG	4007
Crigler-Najjar syndrome 1 Ala368Thr GCC-ACC	TCAGAGATGTAACTGCTGACATCCTCCCTATTTTGCATCTCAG GTCACCCGATGACCCGT**G**CCTTTATCACCCATGCTGGTTCCC ATGGTGTTTATGAAAGCATATGCAATGGCGTTCCCA	4008
	TGGGAACGCCATTGCATATGCTTTCATAAACACCATGGGAAC CAGCATGGGTGATAAAGG**C**ACGGGTCATCGGGTGACCTGAG ATGCAAAATAGGGAGGATGTCAGCAGTTACATCTCTGA	4009
	TGACCCGT**G**CCTTTATC	4010
	GATAAAGG**C**ACGGGTCA	4011
Crigler-Najjar syndrome 1 Ser375Phe TCC-TTC	CCTCCCTATTTTGCATCTCAGGTCACCCGATGACCCGTGCCT TTATCACCCATGCTGGTT**C**CCATGGTGTTTATGAAAGCATATG CAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGG	4012
	CCAAACAAGGGCATCATCACCATGGGAACGCCATTGCATATG CTTTCATAAACACCATGG**G**AACCAGCATGGGTGATAAAGGCA CGGGTCATCGGGTGACCTGAGATGCAAAATAGGGAGG	4013
	TGCTGGTT**C**CCATGGTG	4014
	CACCATGG**G**AACCAGCA	4015
Crigler-Najjar syndrome 1 Ser381Arg AGC-AGG	AGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTC CCATGGTGTTTATGAAAG**C**ATATGCAATGGCGTTCCCATGGT GATGATGCCCTTGTTTGGTGATCAGATGGACAATGCA	4016
	TGCATTGTCCATCTGATCACCAAACAAGGGCATCATCACCAT GGGAACGCCATTGCATAT**G**CTTTCATAAACACCATGGGAACC AGCATGGGTGATAAAGGCACGGGTCATCGGGTGACCT	4017

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TATGAAAG**C**ATATGCAA	4018
	TTGCATAT**G**CTTTCATA	4019
Crigler-Najjar syndrome 1 Ala401Pro GCA-CCA	AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGGTGATCAGATGGACAAT**G**CAAAGCGCATGGAGACTAAGGGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTG	4020
	CAGAAGTCATTTCCAGAACATTCAGGGTCACTCCAGCTCCCTTAGTCTCCATGCGCTTTG**C**ATTGTCCATCTGATCACCAAACAAGGGCATCATCACCATGGGAACGCCATTGCATATGCT	4021
	TGGACAAT**G**CAAAGCGC	4022
	GCGCTTTG**C**ATTGTCCA	4023
Crigler-Najjar syndrome 1 Lys428Glu AAA-GAA	GGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAAGATTTAGAAAATGCTCTA**A**AAGCAGTCATCAATGACAAAAGGTAAGAAAGAAGATACAGAAGAATACTTTGGTCATGGC	4024
	GCCATGACCAAAGTATTCTTCTGTATCTTCTTTCTTACCTTTTGTCATTGATGACTGCTT**T**TAGAGCATTTTCTAAATCTTCAGAAGTCATTTCCAGAACATTCAGGGTCACTCCAGCTCC	4025
	ATGCTCTA**A**AAGCAGTC	4026
	GACTGCTT**T**TAGAGCAT	4027
Crigler-Najjar syndrome 1 Tyr486Asp TAC-GAC	ATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGCAGCCCACGACCTCACCTGGTACCAG**T**ACCATTCCTTGGACGTGATTGGTTTCCTCTTGGCCGTCGTGCTGACAGTGGCCTTCATCA	4028
	TGATGAAGGCCACTGTCAGCACGACGGCCAAGAGGAAACCAATCACGTCCAAGGAATGGT**A**CTGGTACCAGGTGAGGTCGTGGGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGTGCCTCAT	4029
	GGTACCAG**T**ACCATTCC	4030
	GGAATGGT**A**CTGGTACC	4031
Crigler-Najjar syndrome 1 Ser488Phe TCC-TTC	ACAAGGGCGCGCCACACCTGCGCCCCGCAGCCCACGACCTCACCTGGTACCAGTACCATT**C**CTTGGACGTGATTGGTTTCCTCTTGGCCGTCGTGCTGACAGTGGCCTTCATCACCTTTAA	4032
	TTAAAGGTGATGAAGGCCACTGTCAGCACGACGGCCAAGAGGAAACCAATCACGTCCAAG**G**AATGGTACTGGTACCAGGTGAGGTCGTGGGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGT	4033
	GTACCATT**C**CTTGGACG	4034
	CGTCCAAG**G**AATGGTAC	4035

EXAMPLE 23

Alzheimer's Disease - Amyloid precursor protein (APP)

Over the past few decades Alzheimer's disease (AD), once considered a rare disorder, has become recognized as a major public health problem. Although there is no agreement on the exact prevalence of Alzheimer's disease, in part due to difficulties of diagnosis, studies consistently point to an exponential rise in prevalence of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest tasks. Anatomic changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and internal neurofibrillary tangles.

At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with a particular allele of APOE (see Example 20); AD3 is caused by mutation in a gene encoding a 7-transmembrane domain protein, presenilin-1 (PSEN1), and AD4 is caused by mutation in a gene that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2). The attached table discloses the correcting oligonucleotide base sequences for the APP oligonucleotides of the invention.

Table 30

APP Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Glu665Asp GAG-GAC	CTGCATACTTTAATTATGATGTAATACAGGTTCTGGGTTGACA AATATCAAGACGGAGGA**G**ATCTCTGAAGTGAAGATGGATGCA GAATTCCGACATGACTCAGGATATGAAGTTCATCAT	4036
	ATGATGAACTTCATATCCTGAGTCATGTCGGAATTCTGCATCC ATCTTCACTTCAGAGAT**C**TCCTCCGTCTTGATATTTGTCAACC CAGAACCTGTATTACATCATAATTAAAGTATGCAG	4037
	ACGGAGGA**G**ATCTCTGA	4038
	TCAGAGAT**C**TCCTCCGT	4039
Alzheimer disease Ala692Gly GCA-GGA	ATT[illegible]TATTGCATTTAGAAATTAAAATTCTTTTTCTTAATTTGTTTT CAAGGTGTTCTTTG**C**AGAAGATGTGGGTTCAAACAAAGGTGC AATCATTGGACTCATGGTGGGCGGTGTTGTCAT	4040

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTG TTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAATT AAGAAAAAGAATTTTAATTTCTAAATGCAATATAAT	4041
	GTTCTTTGCAGAAGATG	4042
	CATCTTCTGCAAAGAAC	4043
Alzheimer disease Glu693Gln GAA-CAA	TATATTGCATTTAGAAATTAAAATTCTTTTTCTTAATTTGTTTTC AAGGTGTTCTTTGCAGAAGATGTGGGTTCAAACAAAGGTGCA ATCATTGGACTCATGGTGGGCGGTGTTGTCATAG	4044
	CTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTT TGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAA TTAAGAAAAAGAATTTTAATTTCTAAATGCAATATA	4045
	TCTTTGCAGAAGATGTG	4046
	CACATCTTCTGCAAAGA	4047
Alzheimer disease Glu693Gly GAA-GGA	ATATTGCATTTAGAAATTAAAATTCTTTTTCTTAATTTGTTTTCA AGGTGTTCTTTGCAGAAGATGTGGGTTCAAACAAAGGTGCAA TCATTGGACTCATGGTGGGCGGTGTTGTCATAGC	4048
	GCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCT TTGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAA ATTAAGAAAAAGAATTTTAATTTCTAAATGCAATAT	4049
	CTTTGCAGAAGATGTGG	4050
	CCACATCTTCTGCAAAG	4051
Alzheimer disease Ala713Thr GCG-ACG	GAAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATG GTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTG GTGATGCTGAAGAAGAAACAGTACACATCCATTCATC	4052
	GATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGT GATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAG TCCAATGATTGCACCTTTGTTTGAACCCACATCTTC	4053
	TTGTCATAGCGACAGTG	4054
	CACTGTCGCTATGACAA	4055
Schizophrenia Ala713Val GCG-GTG	AAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGG TGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGG TGATGCTGAAGAAGAAACAGTACACATCCATTCATCA	4056
	TGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGG TGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGA GTCCAATGATTGCACCTTTGTTTGAACCCACATCTT	4057
	TGTCATAGCGACAGTGA	4058
	TCACTGTCGCTATGACA	4059
Alzheimer disease Val715Met GTG-ATG	GTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGC GGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATG CTGAAGAAGAAACAGTACACATCCATTCATCATGGTG	4060
	CACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCAC CAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCAC CATGAGTCCAATGATTGCACCTTTGTTTGAACCCAC	4061
	TAGCGACAGTGATCGTC	4062

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GACGATCACTGTCGCTA	4063
Alzheimer disease Ile716Val ATC-GTC	GGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGG	4064
	CCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTGTTTGAACC	4065
	CGACAGTGATCGTCATC	4066
	GATGACGATCACTGTCG	4067
Alzheimer disease Val717Gly GTC-GGC	CAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGGTGGA	4068
	TCCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTGTTTG	4069
	AGTGATCGTCATCACCT	4070
	AGGTGATGACGATCACT	4071
Alzheimer disease Val717Ile GTC-ATC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGGTGG	4072
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4073
	CAGTGATCGTCATCACC	4074
	GGTGATGACGATCACTG	4075
Alzheimer disease Val717Phe GTC-TTC	TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGGTGG	4076
	CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA	4077
	CAGTGATCGTCATCACC	4078
	GGTGATGACGATCACTG	4079
Alzheimer disease Leu723Pro CTG-CCG	TTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCATTCATCATGGTGTGGTGGAGGTAGGTAAACTTGACTG	4080
	CAGTCAAGTTTACCTACCTCCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACCGCCCACCATGAGTCCAA	4081
	GGTGATGCTGAAGAAGA	4082
	TCTTCTTCAGCATCACC	4083

EXAMPLE 24
Alzheimer's Disease - presenilin-1 (PSEN1)

The attached table discloses the correcting oligonucleotide base sequences for the PSEN1 oligonucleotides of the invention.

Table 31
PSEN1 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Ala79Val GCC-GTC	CCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGATGAGGAG CTGACATTGAAATATGGCGCCAAGCATGTGATCATGCTCTTTG TCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC	4084
	GTAGCCACGACCACCACCATGCAGAGAGTCACAGGGACAAA GAGCATGATCACATGCTTGGCGCCATATTTCAATGTCAGCTC CTCATCTTCTTCCTCATCTTGCTCCACCACCTGCCGGG	4085
	ATATGGCGCCAAGCATG	4086
	CATGCTTGGCGCCATAT	4087
Alzheimer disease Val82Leu tGTG-CTG	GTGGTGGAGCAAGATGAGGAAGAAGATGAGGAGCTGACATT GAAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGT GACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGT	4088
	ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTTCAATG TCAGCTCCTCATCTTCTTCCTCATCTTGCTCCACCAC	4089
	CCAAGCATGTGATCATG	4090
	CATGATCACATGCTTGG	4091
Alzheimer disease Val96Phe gGTC-TTC	AAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGTG ACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTC AGCTTTTATACCCGGAAGGATGGGCAGCTGTACGTAT	4092
	ATACGTACAGCTGCCCATCCTTCCGGGTATAAAAGCTGACTG ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTT	4093
	TGGTGGTGGTCGTGGCT	4094
	AGCCACGACCACCACCA	4095
Alzheimer disease Phe105Leu TTTt-TTG	CTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC CATTAAGTCAGTCAGCTTTTATACCCGGAAGGATGGGCAGCT GTACGTATGAGTTTTGTTTTATTATTCTCAAAGCCAG	4096
	CTGGCTTTGAGAATAATAAAACAAAACTCATACGTACAGCTGC CCATCCTTCCGGGTATAAAAGCTGACTGACTTAATGGTAGCC ACGACCACCACCATGCAGAGAGTCACAGGGACAAAG	4097
	GTCAGCTTTTATACCCG	4098
	CGGGTATAAAAGCTGAC	4099

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Thr116Asn ACC-AAC	TGGTGATCTCCATTAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATA**C**CCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGC	4100
	GCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAATGGG**G**TATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTAATGGAGATCACCA	4101
	AATCTATA**C**CCCATTCA	4102
	TGAATGGG**G**TATAGATT	4103
Alzheimer disease Pro117Leu CCA-CTA	TGATCTCCATTAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCC**C**ATTCACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGC	4104
	GCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAAT**G**GGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTAATGGAGATCA	4105
	CTATACCC**C**ATTCACAG	4106
	CTGTGAAT**G**GGGTATAG	4107
Alzheimer disease Glu120Asp GAAg-GAT	TAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCCCATTCACAGA**A**GATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATC	4108
	GATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATC**T**TCTGTGAATGGGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA	4109
	TTCACAGA**A**GATACCGA	4110
	TCGGTATC**T**TCTGTGAA	4111
Alzheimer disease Glu120Asp GAAg-GAC	TAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCCCATTCACAGA**A**GATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATC	4112
	GATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATC**T**TCTGTGAATGGGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA	4113
	TTCACAGA**A**GATACCGA	4114
	TCGGTATC**T**TCTGTGAA	4115
Alzheimer disease Glu120Lys aGAA-AAA	ATTAACACTGACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCCCATTCACA**G**AAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGA	4116
	TCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTT**C**TGTGAATGGGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTAAT	4117
	CATTCACA**G**AAGATACC	4118
	GGTATCTT**C**TGTGAATG	4119
Alzheimer disease Glu123Lys cGAG-AAG	GACCTAGGGCTTTTGTGTTTGTTTTATTGTAGAATCTATACCCCATTCACAGAAGATACC**G**AGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCA	4120

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACAAACACAAAAGCCCTAGGTC	4121
	AAGATACCGAGACTGTG	4122
	CACAGTCTCGGTATCTT	4123
Alzheimer disease Asn135Asp gAAT-GAT	TATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATA	4124
	TATACAGAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATA	4125
	CAATTCTGAATGCTGCC	4126
	GGCAGCATTCAGAATTG	4127
Alzheimer disease Met139Ile ATGa-ATA	AGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTAT	4128
	ATAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCT	4129
	GCCATCATGATCAGTGT	4130
	ACACTGATCATGATGGC	4131
Alzheimer disease Met139Lys ATG-AAG	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4132
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTG	4133
	TGCCATCATGATCAGTG	4134
	CACTGATCATGATGGCA	4135
Alzheimer disease Met139Thr ATG-ACG	CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA	4136
	TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTG	4137
	TGCCATCATGATCAGTG	4138
	CACTGATCATGATGGCA	4139
Alzheimer disease Met139Val cATG-GTG	ACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCT	4140
	AGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCTGT	4141
	CTGCCATCATGATCAGT	4142

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACTGATCA**T**GATGGCAG	4143
Alzheimer disease Ile143Phe cATT-TTT	GAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCT GCCATCATGATCAGTGTC**A**TTGTTGTCATGACTATCCTCCTGG TGGTTCTGTATAAATACAGGTGCTATAAGGTGAGCA	4144
	TGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAG GATAGTCATGACAACAA**T**GACACTGATCATGATGGCAGCATTC AGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCTC	4145
	TCAGTGTC**A**TTGTTGTC	4146
	GACAACAA**T**GACACTGA	4147
Alzheimer disease Ile143Thr ATT-ACT	AGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTG CCATCATGATCAGTGTCA**T**TGTTGTCATGACTATCCTCCTGGT GGTTCTGTATAAATACAGGTGCTATAAGGTGAGCAT	4148
	ATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGA GGATAGTCATGACAACA**A**TGACACTGATCATGATGGCAGCAT TCAGAATTGAGTGCAGGGCTCTCTGGCCCACAGTCT	4149
	CAGTGTCA**T**TGTTGTCA	4150
	TGACAACA**A**TGACACTG	4151
Alzheimer disease Met146Ile ATGa-ATA	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCATTGTTGTCAT**G**ACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4152
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT**C**ATGACAACAATGACACTGATCATG ATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGG	4153
	GTTGTCAT**G**ACTATCCT	4154
	AGGATAGT**C**ATGACAAC	4155
Alzheimer disease Met146Ile ATGa-ATC	CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCATTGTTGTCAT**G**ACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA	4156
	TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT**C**ATGACAACAATGACACTGATCATG ATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGG	4157
	GTTGTCAT**G**ACTATCCT	4158
	AGGATAGT**C**ATGACAAC	4159
Alzheimer disease Met146Leu cATG-TTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCATTGTTGTC**A**TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4160
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCA**T**GACAACAATGACACTGATCATGAT GGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCC	4161
	TTGTTGTC**A**TGACTATC	4162
	GATAGTCA**T**GACAACAA	4163
Alzheimer disease Met146Val cATG-GTG	GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCATTGTTGTC**A**TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA	4164

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCA**T**GACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCTGGCC	4165
	TTGTTGTC**A**TGACTATC	4166
	GATAGTCA**T**GACAACAA	4167
Alzheimer disease Thr147Ile ACT-ATT	AGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGA**C**TATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTATAAGGTGAGCATGAGACACAGATC	4168
	GATCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAGGATA**G**TCATGACAACAATGACACTGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCT	4169
	TGTCATGA**C**TATCCTCC	4170
	GGAGGATA**G**TCATGACA	4171
Alzheimer disease His163Arg CAT-CGT	CTTTTTAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCC**A**TGCCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGG	4172
	CCCAAGTAAATGAATGAAAAAAAGAACAGCAACAATAGAGATGATATAATAAGCCAGGCA**T**GGATGACCTAGAAAAGAAAGCATTTCAATATAATTAACAGGTCCCACAACCCTTAAAAAG	4173
	GGTCATCC**A**TGCCTGGC	4174
	GCCAGGCA**T**GGATGACC	4175
Alzheimer disease His163Tyr cCAT-TAT	ACTTTTTAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATC**C**ATGCCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGG	4176
	CCAAGTAAATGAATGAAAAAAAGAACAGCAACAATAGAGATGATATAATAAGCCAGGCAT**G**GATGACCTAGAAAAGAAAGCATTTCAATATAATTAACAGGTCCCACAACCCTTAAAAAGT	4177
	AGGTCATC**C**ATGCCTGG	4178
	CCAGGCAT**G**GATGACCT	4179
Alzheimer disease Trp165Cys TGGc-TGC	AGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTG**G**CTTATTATATCATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGTAAGTT	4180
	AACTTACCCCAAGTAAATGAATGAAAAAAAGAACAGCAACAATAGAGATGATATAATAAG**C**CAGGCATGGATGACCTAGAAAAGAAAGCATTTCAATATAATTAACAGGTCCCACAACCCT	4181
	CATGCCTG**G**CTTATTAT	4182
	ATAATAAG**C**CAGGCATG	4183
Alzheimer disease Ser169Leu TCA-TTA	ACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATTATAT**C**ATCTCTATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGTAAGTTGTGAAATTTTT	4184
	AAAAATTTCACAACTTACCCCAAGTAAATGAATGAAAAAAAGAACAGCAACAATAGAGAT**G**ATATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCATTTCAATATAATTAACAGGT	4185
	TATTATAT**C**ATCTCTAT	4186

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ATAGAGAT**G**ATATAATA	4187
Alzheimer disease Leu171Pro CTA-CCA	TAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATTATATCATCTC**T**ATTGTTGCTGTTCTTTTTTTCATTCATTTACTTGGGGTAAGTTGTGAAATTTTTGGTCTG	4188
	CAGACCAAAAATTTCACAACTTACCCCAAGTAAATGAATGAAAAAAAGAACAGCAACAAT**A**GAGATGATATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCATTTCAATATAATTA	4189
	ATCATCTC**T**ATTGTTGC	4190
	GCAACAAT**A**GAGATGAT	4191
Alzheimer disease Leu173Trp TTG-TGG	TATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATTATATCATCTCTATTGT**T**GCTGTTCTTTTTTTCATTCATTTACTTGGGGTAAGTTGTGAAATTTTTGGTCTGTCTTTC	4192
	GAAAGACAGACCAAAAATTTCACAACTTACCCCAAGTAAATGAATGAAAAAAAGAACAGC**A**ACAATAGAGATGATATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCATTTCAATA	4193
	TCTATTGT**T**GCTGTTCT	4194
	AGAACAGC**A**ACAATAGA	4195
Alzheimer disease Gly209Arg gGGA-AGA	TATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTG**G**GAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGA	4196
	TCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTC**C**CACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTATA	4197
	GTGTGGTG**G**GAATGATT	4198
	AATCATTC**C**CACCACAC	4199
Alzheimer disease Gly209Val GGA-GTA	ATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGG**G**AATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGAT	4200
	ATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATT**C**CCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTAT	4201
	TGTGGTGG**G**AATGATTT	4202
	AAATCATT**C**CCACCACA	4203
Alzheimer disease Ile213Thr ATT-ACT	TGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCA**T**TCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCAT	4204
	ATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGA**A**TGGAAATCATTCCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCA	4205
	GATTTCCA**T**TCACTGGA	4206
	TCCAGTGA**A**TGGAAATC	4207
Alzheimer disease Leu219Pro CTT-CCT	CACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCAC**T**TCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAA	4208

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGA**A**GTGGACCTTTCCAGTGAATGGAAATCATTCCCACCACACCAAAATTCCAGATCAGGAGTG	4209
	AGGTCCAC**T**TCGACTCC	4210
	GGAGTCGA**A**GTGGACCT	4211
Alzheimer disease Ala231Thr tGCC-ACC	ATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGT**G**CCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGG	4212
	CCAAGATGAGCCACGCAGTCCATTCAGGGAGGTACTTGATAAACACCAGGGCCATGAGGG**C**ACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAAT	4213
	TGATTAGT**G**CCCTCATG	4214
	CATGAGGG**C**ACTAATCA	4215
Alzheimer disease Ala231Val GCC-GTC	TTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTG**C**CCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGC	4216
	GCCAAGATGAGCCACGCAGTCCATTCAGGGAGGTACTTGATAAACACCAGGGCCATGAGG**G**CACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAA	4217
	GATTAGTG**C**CCTCATGG	4218
	CCATGAGG**G**CACTAATC	4219
Alzheimer disease Met233Thr ATG-ACG	TTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCA**T**GGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGAT	4220
	ATCACAGCCAAGATGAGCCACGCAGTCCATTCAGGGAGGTACTTGATAAACACCAGGGCC**A**TGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAA	4221
	TGCCCTCA**T**GGCCCTGG	4222
	CCAGGGCC**A**TGAGGGCA	4223
Alzheimer disease Leu235Pro CTG-CCG	GGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCATGGCCC**T**GGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGT	4224
	ACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTCAGGGAGGTACTTGATAAACACC**A**GGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCC	4225
	CATGGCCC**T**GGTGTTTA	4226
	TAAACACC**A**GGGCCATG	4227
Alzheimer disease Ala246Glu GCG-GAG	TCATTATGATTAGTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTG**C**GTGGCTCATCTTGGCTGTGATTTCAGTATATGGTAAAACCCAAGACTGATAATTTGTTTG	4228
	CAAACAAATTATCAGTCTTGGGTTTTACCATATACTGAAATCACAGCCAAGATGAGCCAC**G**CAGTCCATTCAGGGAGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGA	4229
	ATGGACTG**C**GTGGCTCA	4230

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	TGAGCCACGCAGTCCAT	4231
Alzheimer disease Leu250Ser TTG-TCG	GTGCCCTCATGGCCCTGGTGTTTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAGTATATGGTAAAACCCAAGACTGATAATTTGTTTGTCACAGGAATGC	4232
	GCATTCCTGTGACAAACAAATTATCAGTCTTGGGTTTTACCATATACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTCAGGGAGGTACTTGATAAACACCAGGGCCATGAGGGCAC	4233
	GCTCATCTTGGCTGTGA	4234
	TCACAGCCAAGATGAGC	4235
Alzheimer disease Ala260Val GCT-GTT	AGTTTAGCCCATACATTTTATTAGATGTCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGA	4236
	TCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGACATCTAATAAAATGTATGGGCTAAACT	4237
	TTTAGTGGCTGTTTTGT	4238
	ACAAAACAGCCACTAAA	4239
Alzheimer disease Leu262Phe TTGt-TTC	CCCATACATTTTATTAGATGTCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTT	4240
	AAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGACATCTAATAAAATGTATGGG	4241
	GCTGTTTTGTGTCCGAA	4242
	TTCGGACACAAAACAGC	4243
Alzheimer disease Cys263Arg gTGT-CGT	CCATACATTTTATTAGATGTCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTT	4244
	AAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGACATCTAATAAAATGTATGG	4245
	CTGTTTTGTGTCCGAAA	4246
	TTTCGGACACAAAACAG	4247
Alzheimer disease Pro264Leu CCG-CTG	ACATTTTATTAGATGTCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTCC	4248
	GGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGACATCTAATAAAATGT	4249
	TTTGTGTCCGAAAGGTC	4250
	GACCTTTCGGACACAAA	4251
Alzheimer disease Arg269Gly tCGT-GGT	GTCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTCCAGCTCTCATTTACT	4252

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	AGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATAC**G**AAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGAC	4253
	GTCCACTT**C**GTATGCTG	4254
	CAGCATAC**G**AAGTGGAC	4255
Alzheimer disease Arg269His CGT-CAT	TCTTTTATGTTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTC**G**TATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTTCCAGCTCTCATTTACTC	4256
	GAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATA**C**GAAGTGGACCTTTCGGACACAAAACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGA	4257
	TCCACTTC**G**TATGCTGG	4258
	CCAGCATA**C**GAAGTGGA	4259
Alzheimer disease Arg278Thr AGA-ACA	TAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGA**G**AAATGAAACGCTTTTTCCAGCTCTCATTTACTCCTGTAAGTATTTGAGAATGATATTGAA	4260
	TTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTT**C**TCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAGCCACTA	4261
	TCAGGAGA**G**AAATGAAA	4262
	TTTCATTT**C**TCTCCTGA	4263
Alzheimer disease Glu280Ala GAA-GCA	CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATG**A**AACGCTTTTTCCAGCTCTCATTTACTCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4264
	TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTT**T**CATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAG	4265
	GAGAAATG**A**AACGCTTT	4266
	AAAGCGTT**T**CATTTCTC	4267
Alzheimer disease Glu280Gly GAA-GGA	CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATG**A**AACGCTTTTTCCAGCTCTCATTTACTCCTGTAAGTATTTGAGAATGATATTGAATTAGTA	4268
	TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAAAGCGTT**T**CATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACAAAACAG	4269
	GAGAAATG**A**AACGCTTT	4270
	AAAGCGTT**T**CATTTCTC	4271
Alzheimer disease Leu282Arg CTT-CGT	TGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAATGAAACGC**T**TTTTCCAGCTCTCATTTACTCCTGTAAGTATTTGAGAATGATATTGAATTAGTAATCAGT	4272
	ACTGATTACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTGGAAAA**A**GCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGACCTTTCGGACACA	4273
	TGAAACGC**T**TTTTCCAG	4274

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	CTGGAAAA**A**GCGTTTCA	4275
Alzheimer disease Ala285Val GCT-GTT	AAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAA ATGAAACGCTTTTTCCAG**C**TCTCATTTACTCCTGTAAGTATTTG AGAATGATATTGAATTAGTAATCAGTGTAGAATTT	4276
	AAATTCTACACTGATTACTAATTCAATATCATTCTCAAATACTTA CAGGAGTAAATGAGA**G**CTGGAAAAAGCGTTTCATTTCTCTCCT GAGCTGTTTCAACCAGCATACGAAGTGGACCTT	4277
	TTTTCCAG**C**TCTCATTT	4278
	AAATGAGA**G**CTGGAAAA	4279
Alzheimer disease Leu286Val tCTC-GTC	GGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAAT GAAACGCTTTTTCCAGCT**C**TCATTTACTCCTGTAAGTATTTGA GAATGATATTGAATTAGTAATCAGTGTAGAATTTAT	4280
	ATAAATTCTACACTGATTACTAATTCAATATCATTCTCAAATACT TACAGGAGTAAATGA**G**AGCTGGAAAAAGCGTTTCATTTCTCTC CTGAGCTGTTTCAACCAGCATACGAAGTGGACC	4281
	TTCCAGCT**C**TCATTTAC	4282
	GTAAATGA**G**AGCTGGAA	4283
Alzheimer disease Gly384Ala GGA-GCA	GTGACCAACTTTTTAATATTTGTAACCTTTCCTTTTTAGGGGGA GTAAAACTTGGATTGG**G**AGATTTCATTTTCTACAGTGTTCTGG TTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTG	4284
	CAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACA CTGTAGAAAATGAAATCT**C**CCAATCCAAGTTTTACTCCCCCTA AAAAGGAAAGGTTACAAATATTAAAAAGTTGGTCAC	4285
	TGGATTGG**G**AGATTTCA	4286
	TGAAATCT**C**CCAATCCA	4287
Alzheimer disease Ser390Ile AGT-ATT	TTTGTAACCTTTCCTTTTTAGGGGGAGTAAAACTTGGATTGGG AGATTTCATTTTCTACA**G**TGTTCTGGTTGGTAAAGCCTCAGCA ACAGCCAGTGGAGACTGGAACACAACCATAGCCTG	4288
	CAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAG GCTTTACCAACCAGAACA**C**TGTAGAAAATGAAATCTCCCAATC CAAGTTTTACTCCCCCTAAAAAGGAAAGGTTACAAA	4289
	TTTCTACA**G**TGTTCTGG	4290
	CCAGAACA**C**TGTAGAAA	4291
Alzheimer disease Leu392Val tCTG-GTG	AACCTTTCCTTTTTAGGGGGAGTAAAACTTGGATTGGGAGATT TCATTTTCTACAGTGTT**C**TGGTTGGTAAAGCCTCAGCAACAGC CAGTGGAGACTGGAACACAACCATAGCCTGTTTCG	4292
	CGAAACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTG CTGAGGCTTTACCAACCA**G**AACACTGTAGAAAATGAAATCTCC CAATCCAAGTTTTACTCCCCCTAAAAAGGAAAGGTT	4293
	ACAGTGTT**C**TGGTTGGT	4294
	ACCAACCA**G**AACACTGT	4295
Alzheimer disease Asn405Ser AAC-AGC	ATTTCATTTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCAAC AGCCAGTGGAGACTGGA**A**CACAACCATAGCCTGTTTCGTAGC CATATTAATTGTAAGTATACACTAATAAGAATGTGT	4296

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	ACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAAACAGGCTATGGTTGTG**T**TCCAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACACTGTAGAAAATGAAAT	4297
	AGACTGGA**A**CACAACCA	4298
	TGGTTGTG**T**TCCAGTCT	4299
Alzheimer disease Ala409Thr aGCC-ACC	TACAGTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATA**G**CCTGTTTCGTAGCCATATTAATTGTAAGTATACACTAATAAGAATGTGTCAGAGCTCTTA	4300
	TAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAAACAGG**C**TATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACACTGTA	4301
	CAACCATA**G**CCTGTTTC	4302
	GAAACAGG**C**TATGGTTG	4303
Alzheimer disease Cys410Tyr TGT-TAT	GTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTGGAACACAACCATAGCCT**G**TTTCGTAGCCATATTAATTGTAAGTATACACTAATAAGAATGTGTCAGAGCTCTTAATGT	4304
	ACATTAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAAA**C**AGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACAC	4305
	CATAGCCT**G**TTTCGTAG	4306
	CTACGAAA**C**AGGCTATG	4307
Alzheimer disease Ala426Pro tGCC-CCC	TGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTGTGCCTTACATTATTACTCCTT**G**CCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTTCT	4308
	AGAAAACAAGCCCAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTGAAAATGG**C**AAGGAGTAATAATGTAAGGCACAAACCCTGTGGAGAAGATGGGAAAGACACACATTCACA	4309
	TACTCCTT**G**CCATTTTC	4310
	GAAAATGG**C**AAGGAGTA	4311
Alzheimer disease Pro436Gln CCA-CAA	AGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTC**C**AATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTTT	4312
	AAAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGCCCAAAGGTGATGGAGATT**G**GAAGAGCTGGCAATGCTTTCTTGAAAATGGCAAGGAGTAATAATGTAAGGCACAAACCCT	4313
	AGCTCTTC**C**AATCTCCA	4314
	TGGAGATT**G**GAAGAGCT	4315
Alzheimer disease Pro436Ser tCCA-TCA	CAGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTT**C**CAATCTCCATCACCTTTGGGCTTGTTTTCTACTTTGCCACAGATTATCTTGTACAGCCTT	4316
	AAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGCCCAAAGGTGATGGAGATTG**G**AAGAGCTGGCAATGCTTTCTTGAAAATGGCAAGGAGTAATAATGTAAGGCACAAACCCTG	4317
	CAGCTCTT**C**CAATCTCC	4318

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GGAGATTGGAAGAGCTG	4319

EXAMPLE 25
Alzheimer's Disease - presenilin-2 (PSEN2)

The attached table discloses the correcting oligonucleotide base sequences for the PSEN2 oligonucleotides of the invention.

Table 32
PSEN2 Mutations and Genome-Correcting Oligos

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
Alzheimer disease Arg62His CGC-CAC	GATGTGGTTTCCCACAGAGAAGCCAGGAGAACGAGGAGGAC GGTGAGGAGGACCCTGACCGCTATGTCTGTAGTGGGGTTCC CGGGCGGCCGCCAGGCCTGGAGGAAGAGCTGACCCTCAA	4320
	TTGAGGGTCAGCTCTTCCTCCAGGCCTGGCGGCCGCCCGGG AACCCCACTACAGACATAGCGGTCAGGGTCCTCCTCACCGTC CTCCTCGTTCTCCTGGCTTCTCTGTGGGAAACCACATC	4321
	CCCTGACCGCTATGTCT	4322
	AGACATAGCGGTCAGGG	4323
Alzheimer disease Thr122Pro cACG-CCG	GCCTCGAGGAGCAGTCAGGGCCGGGAGCATCAGCCCTTTGC CTTCTCCCTCAGCATCTACACGACATTCACTGAGGACACACC CTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACA	4324
	TGTTCAGCACGGAGTTGAGGAGGCGCTGGCCCACCGAGGGT GTGTCCTCAGTGAATGTCGTGTAGATGCTGAGGGAGAAGGCA AAGGGCTGATGCTCCCGGCCCTGACTGCTCCTCGAGGC	4325
	GCATCTACACGACATTC	4326
	GAATGTCGTGTAGATGC	4327
Alzheimer disease Asn141Ile AAC-ATC	ACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGCGC CTCCTCAACTCCGTGCTGAACACCCTCATCATGATCAGCGTC ATCGTGGTTATGACCATCTTCTTGGTGGTGCTCTACAA	4328
	TTGTAGAGCACCACCAAGAAGATGGTCATAACCACGATGACG CTGATCATGATGAGGGTGTTCAGCACGGAGTTGAGGAGGCG CTGGCCCACCGAGGGTGTGTCCTCAGTGAATGGCGTGT	4329
	CGTGCTGAACACCCTCA	4330
	TGAGGGTGTTCAGCACG	4331
Alzheimer disease Met239Ile ATGg-ATA	CCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCA TCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTACCT CCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCATC	4332

Clinical Phenotype & Mutation	Correcting Oligos	SEQ ID NO:
	GATGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGT ACTTGATGAACACTAGGGCCATGAGCGCACTGATCATGATGA GGTAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGG	4333
	GCGCTCATGGCCCTAGT	4334
	ACTAGGGCCATGAGCGC	4335
Alzheimer disease Met239Val cATG-GTG	ATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCT CATCATGATCAGTGCGCTCATGGCCCTAGTGTTCATCAAGTA CCTCCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCA	4336
	TGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGTAC TTGATGAACACTAGGGCCATGAGCGCACTGATCATGATGAGG TAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGGAT	4337
	GTGCGCTCATGGCCCTA	4338
	TAGGGCCATGAGCGCAC	4339

EXAMPLE 26
Plant Cells

The oligonucleotides of the invention can also be used to repair or direct a mutagenic event in plants and animal cells. Although little information is available on plant mutations amongst natural cultivars, the oligonucleotides of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying Gln can be modified at a specific site to TAA; a AAG codon specifying Lys can be modified to UAG at a specific site; and a CGA codon for Arg can be modified to a UGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a defective truncated protein, shortened at the site of the stop codon. Alternatively, frameshift additions or deletions can be directed into the genome at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. An oligonucleotide for targeted alteration(s) of genetic sequence, comprising a single-stranded oligonucleotide having a DNA domain, said DNA domain having at least one mismatch with respect to the genetic sequence to be altered, and further comprising chemical modifications within the oligonucleotide, said targeted alteration(s) occurring more frequently than alteration(s) of the genetic sequence by a double-stranded double hairpin chimeric oligonucleotide containing RNA and DNA nucleotides.

2. The oligonucleotide according to claim one that comprises at least one phosphorothioate linkage within the oligonucleotide.

3. The oligonucleotide according to claim one that comprises a 2'-O-methyl analog.

4. The oligonucleotide according to claim one that comprises a locked nucleotide analog.

5. The oligonucleotide according to claim one that comprises a combination of at least two modifications selected from the group of a phosphorothioate linkage, a 2'-O-methyl analog, a locked nucleotide analog and a ribonucleotide.

6. The oligonucleotide according to any one of claims 1 to 5 that comprises at least one unmodified ribonucleotide.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the sequence of said oligonucleotide is selected from the group consisting of SEQ ID NOS: 1-4340.

8. A method of targeted alteration of genetic material, comprising combining the target genetic material with an oligonucleotide according to any one of claims 1 to 7 in the presence of purified proteins.

9. A method of targeted alteration of genetic material, comprising administering to a cell extract an oligonucleotide of any one of claims 1 to 7.

10. A method of targeted alteration of genetic material, comprising administering to a cell an oligonucleotide of any one of claims 1 to 7.

11. A method of targeted alteration of genetic sequence in a subject, comprising administering to the subject an oligonucleotide of any one of claims 1 to 7.

12. A method of targeted alteration of genetic sequence, comprising combining target genetic material with an oligonucleotide according to any one of claims 1 to 7, said target genetic material being a non-transcribed DNA strand of a duplex DNA.

13. The genetic material obtained by any one of the methods of claim 8, 9 or claim 10.

14. A cell comprising the genetic material of claim 13.

15. A non-human organism comprising the cell according to claim 14.

16. A pharmaceutical composition comprising the oligonucleotide according to any one of claims 1 to 7.

17. A method of targeted chromosomal genomic alteration, comprising administering the pharmaceutical composition of claim 16 to a subject.

18. A non-human organism produced by the method of claim 11 or claim 17.

19. A method of optimizing an oligonucleotide for targeted alteration of a genetic sequence, which comprises:

(a) comparing the efficiency of alteration of a targeted genetic sequence by an oligonucleotide of any one of claims 1 to 7 with the efficiency of alteration of the same targeted genetic sequence by a

second oligonucleotide, said second oligonucleotide selected from the group of (1) an oligonucleotide that is fully complementary to the target and lacks the mismatch, (2) a fully modified phosphorothiolated oligonucleotide, (3) a fully modified 2'-O-methylated oligonucleotide and (4) a chimeric double-stranded double hairpin containing RNA and DNA nucleotides.

20. The method of claim 19 in which the alteration is produced in a cell extract.

21. The method of claim 20 in which the cell extract is selected from the group of a fungal cell extract, a plant cell extract, a rodent cell extract, a primate cell extract and a human cell extract.

22. The method of claim 19 in which the alteration is produced in a cell.

23. The method of claim 21 in which the cell is selected from the group of a fungal cell, a plant cell, a rodent cell, a primate cell and a human cell.

24. A kit comprising the oligonucleotide according to any one of claims 1 to 7 and a second oligonucleotide selected from the group of (1) an oligonucleotide that is fully complementary to the target and lacks the mismatch, (2) a fully modified phosphorothiolated oligonucleotide, (3) a fully modified 2-O-methylated oligonucleotide and (4) a chimeric double stranded double hairpin containing RNA and DNA nucleotides.

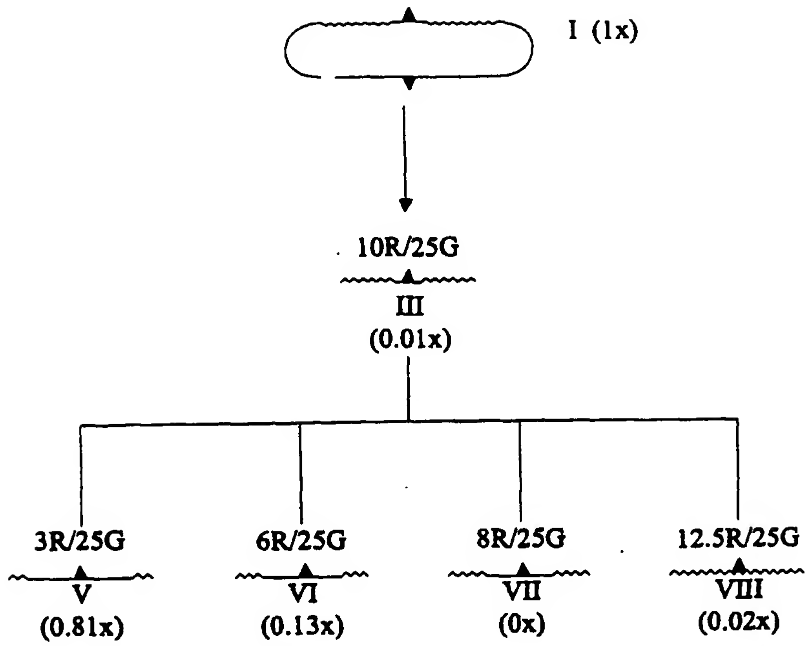


Figure 1A

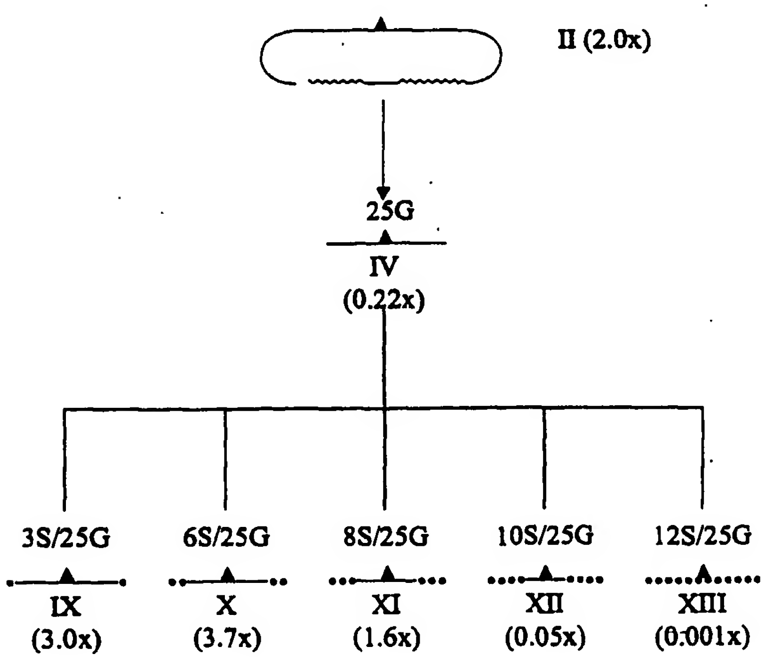


Figure 1B

2/12

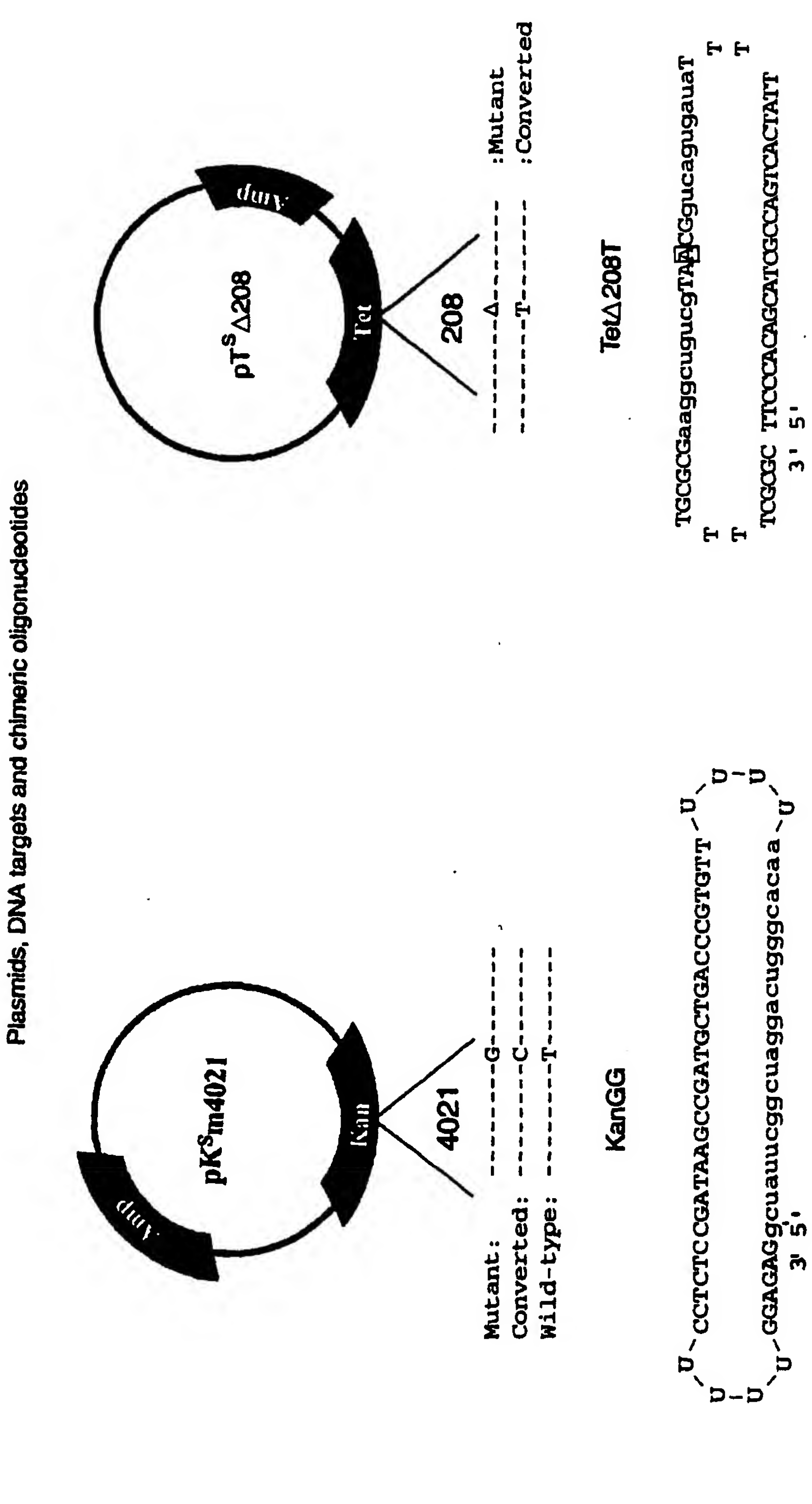


Figure 1C

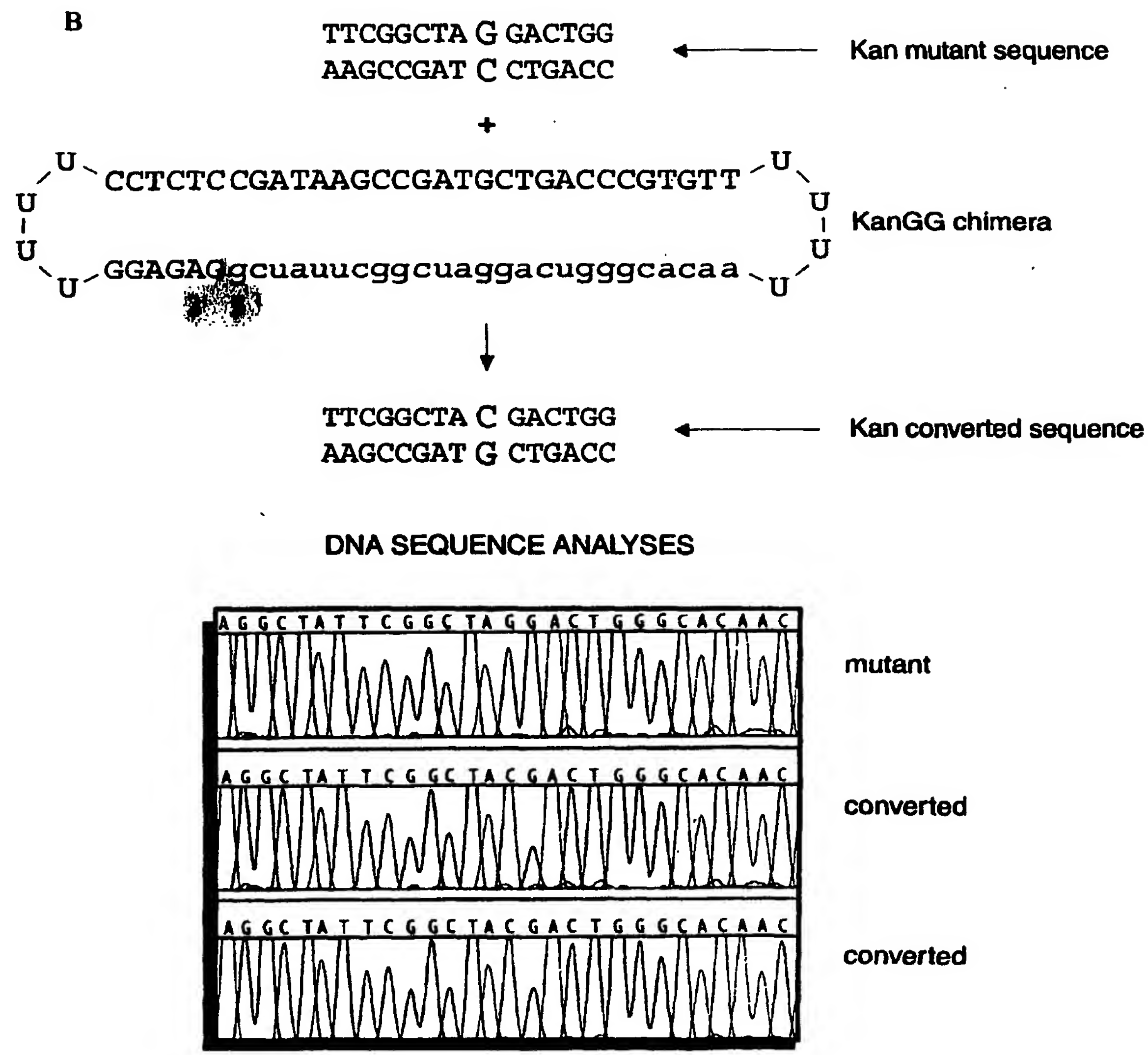

B
TTCGGCTA G GACTGG
AAGCCGAT C CTGACC
Kan mutant sequence
+
CCTCTCCGATAAGCCGATGCTGACCCGTGTT
GGAGAGgcuauucggcuaggacugggcacaa
U U U U U U U U
KanGG chimera
TTCGGCTA C GACTGG
AAGCCGAT G CTGACC
Kan converted sequence
DNA SEQUENCE ANALYSES
AGGCTATTCGGCTAGGACTGGGCACAAC
mutant
AGGCTATTCGGCTACGACTGGGCACAAC
converted
AGGCTATTCGGCTACGACTGGGCACAAC
converted

Figure 1D

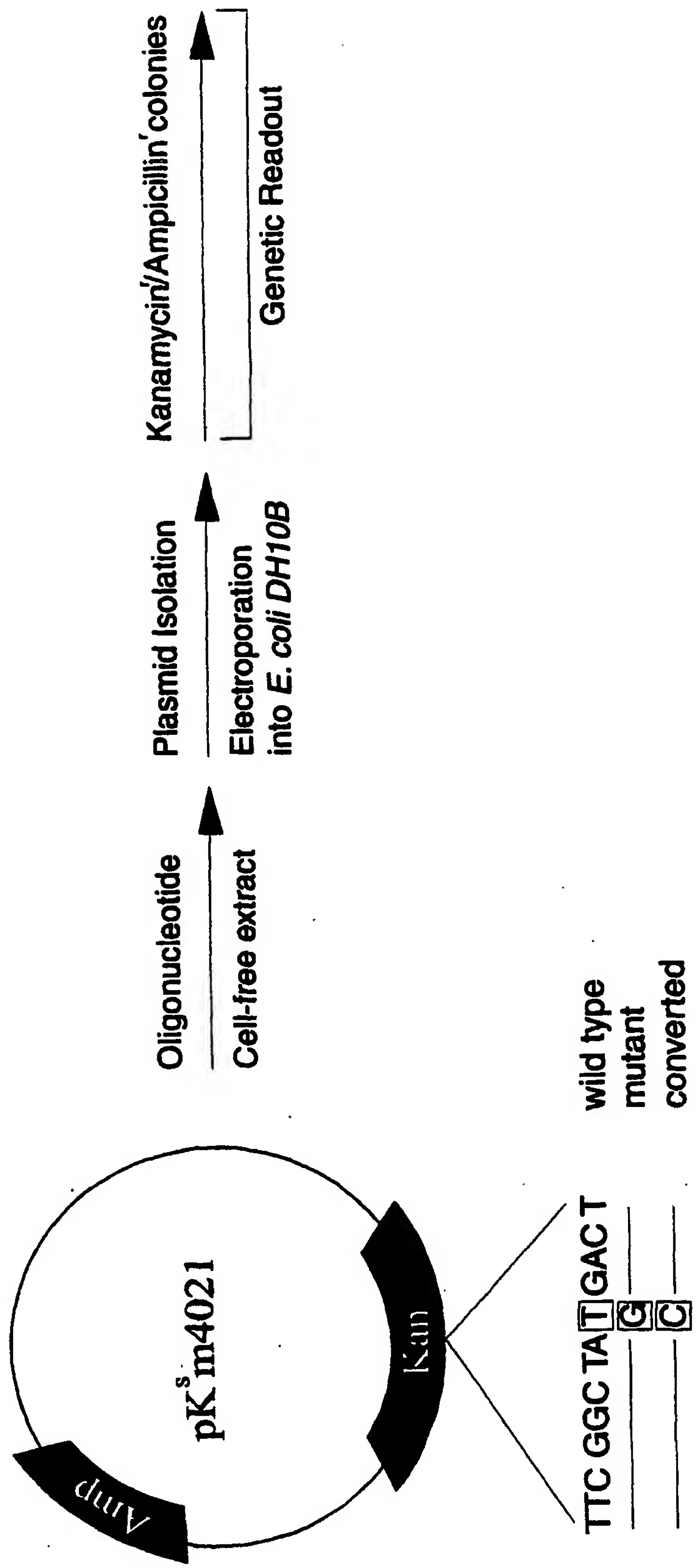
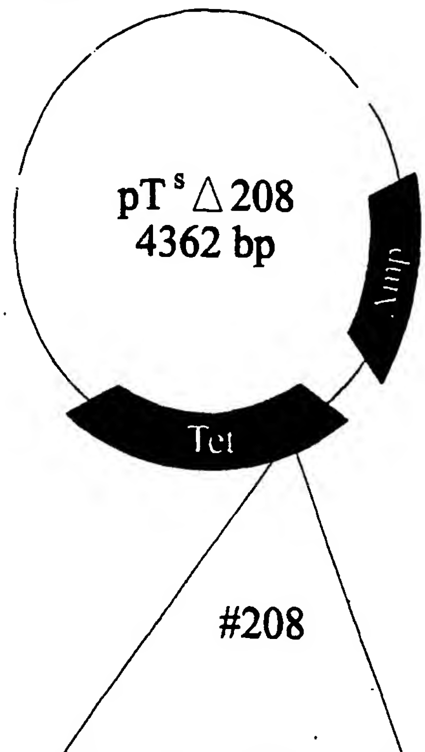

Oligonucleotide
Cell-free extract
Plasmid Isolation
Electroporation into E. coli DH10B
Kanamycin^r/Ampicillin^r colonies
Genetic Readout
pK^s m4021
Kan
Amp
TTC GGC TA T GAC T
G
C
wild type
mutant
converted

Figure 2



Wild type: GAC AGC AT $\boxed{C}$ GCCAGT
Mutant: GAC AGC AT - GCCAGT
Converted: GAC AGC AT $\boxed{T}$ GCCAGT

Sequence analysis of Tet^r plasmid Δ208

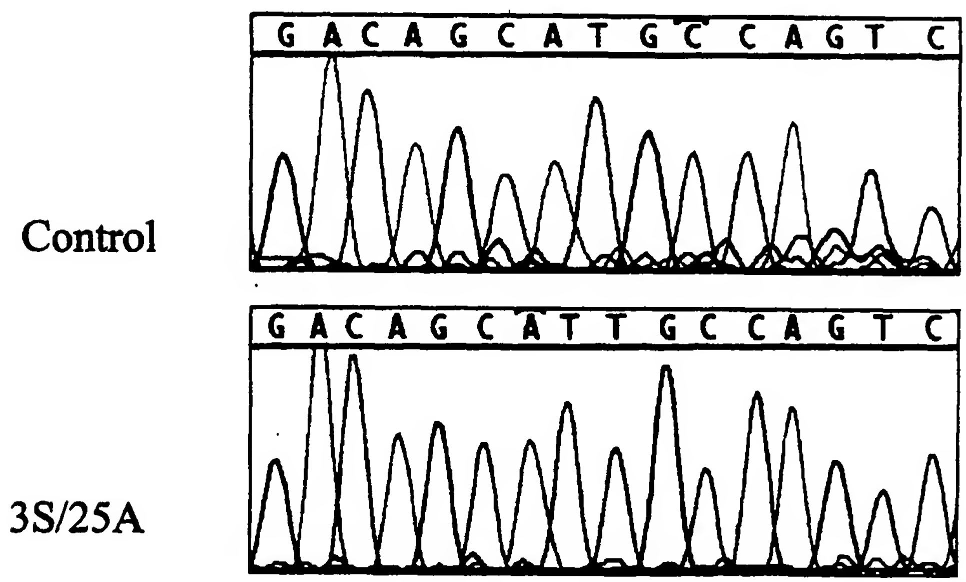


Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distribution

oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)	—	+	—	—	—
2) 6S/25G (20)	—	+	—	—	—
3) 8S/25G (20)	—	+	—	—	—
4) 10S/25G (18)	—	+	—	+(2)	+(2)
5) 25S/25G (4)	—	—	+(2)	+(2)	—

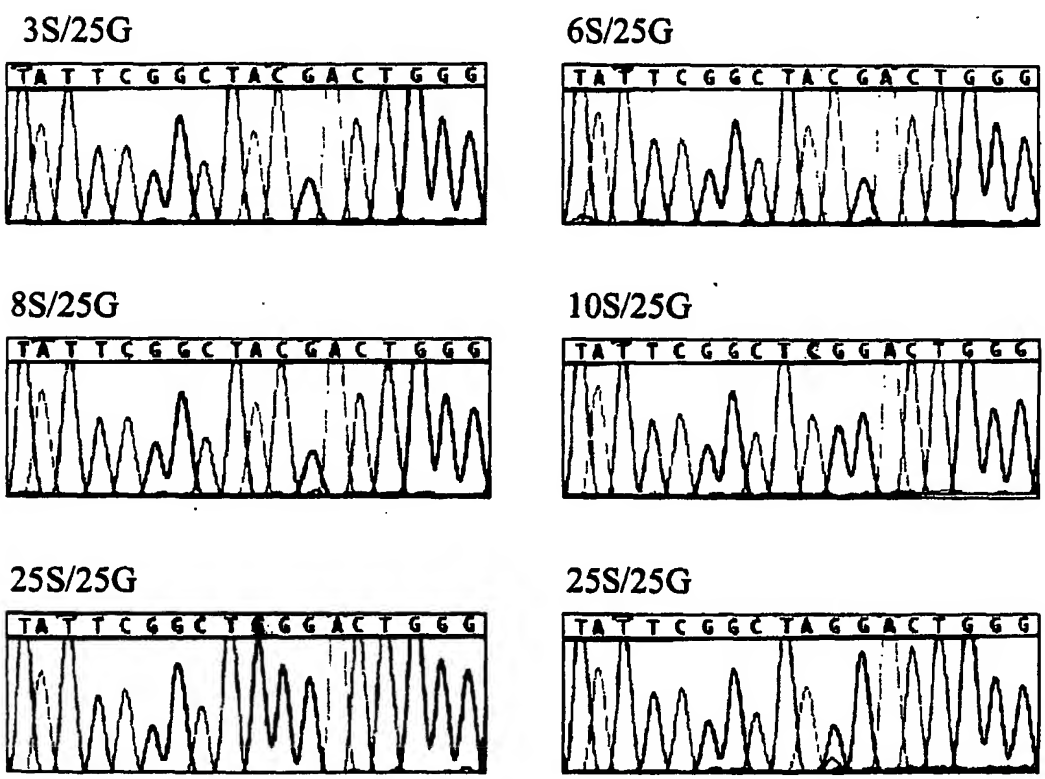


Figure 4

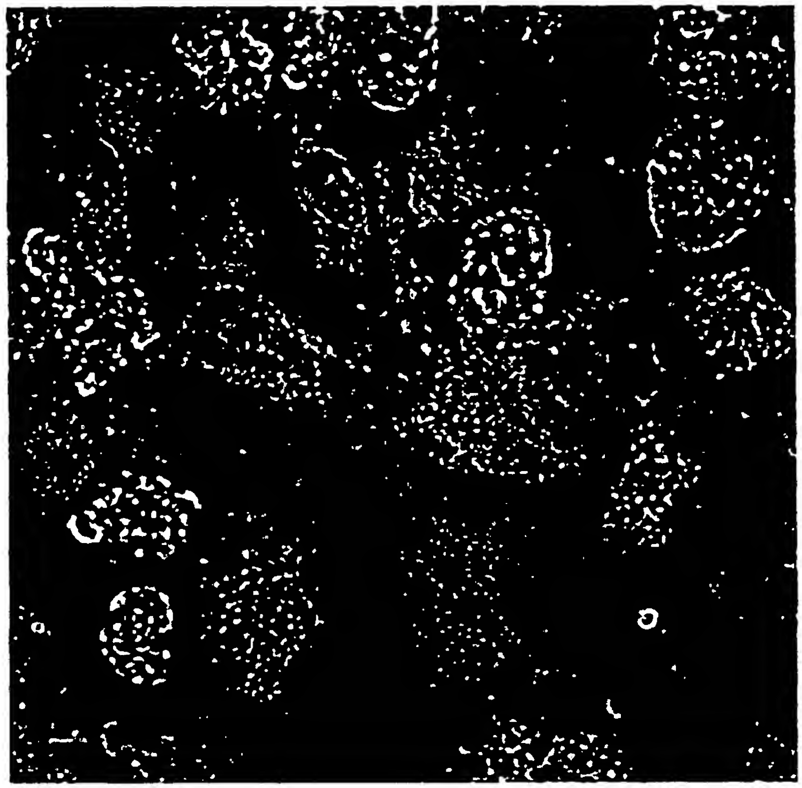


Figure 5

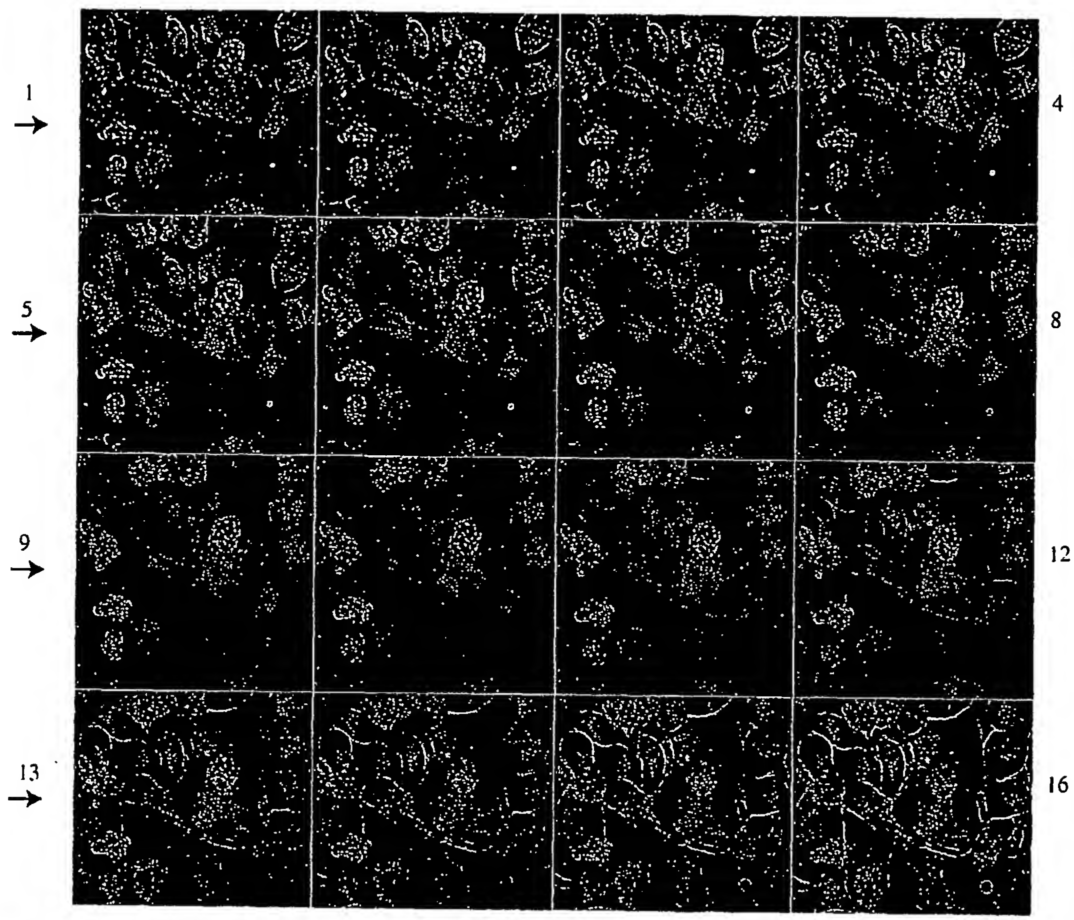


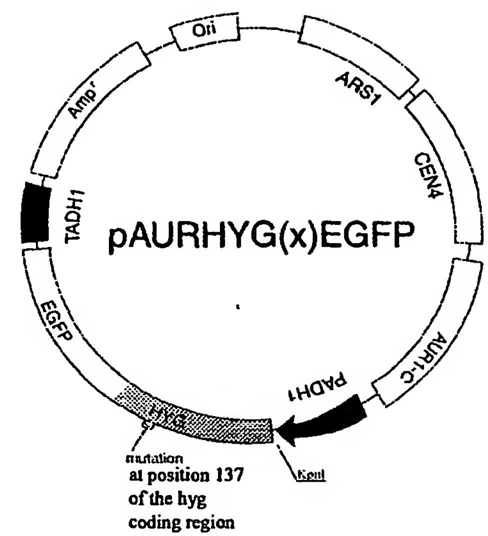
Figure 6

Sequence of normal allele: GTGGATATGTCCT
Target/existing mutant: GTGGATAATGTCCT
Desired alteration: GTGGATACGTCCT

Figure 7A

Sequence of normal allele: GTGGATATGTCCT
Target/existing mutant: GTGGATAGGTCCT
Desired alteration: GTGGATACGTCCT

Figure 7B



HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

HygE3T/74: 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3'

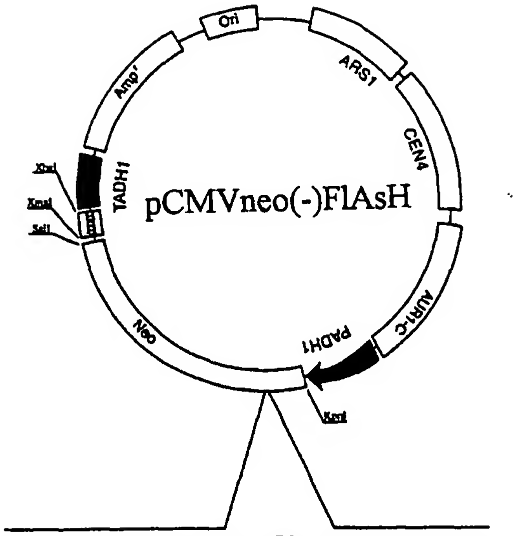
HygE3T/74α: 5'-GTA GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC ACG AG-3'

HygGG/Rev:

```
  T                                     T
 / \                                   / \
T   ACATCCTCCCGCACCTATGCAGGACGCCCAT     T
T   TGTAGGagggcguggaTAGGTccugcgggua     T
 \ /       / \                         \ /
  T     3'    5'                        T
```

Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



TTCGGCTA G GACTGG
AAGCCGAT C CTGACC

Neo/kan target mutant

TTCGGCTA C GACTGG
AAGCCGAT G CTGACC

converted

FUSION GENE FOR LIGAND BINDING

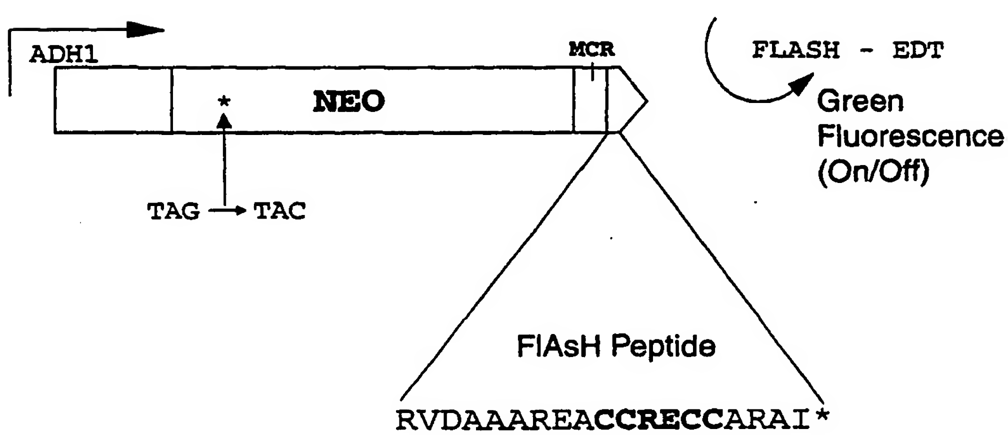


Figure 9

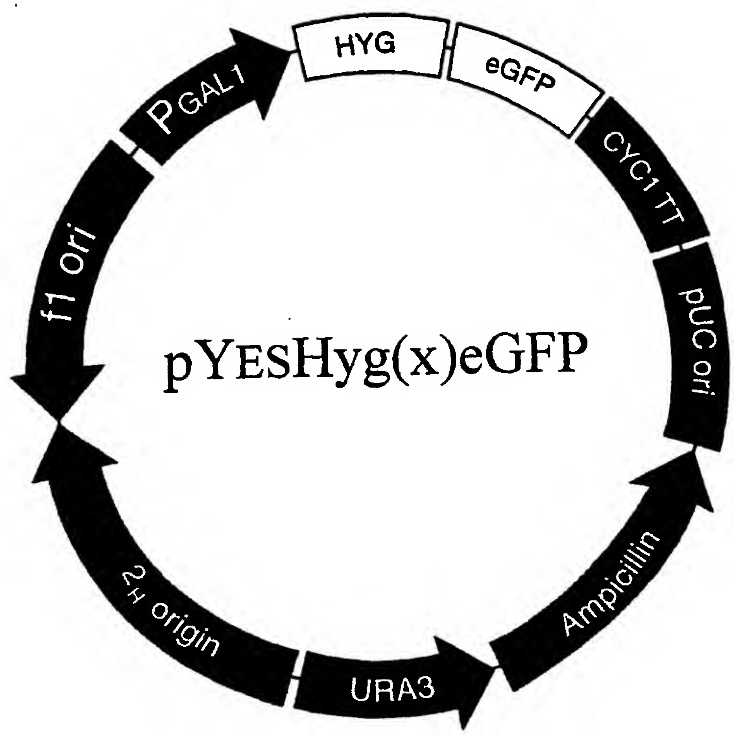

HYG
eGFP
CYC1 TT
pUC ori
Ampicillin
URA3
2μ origin
f1 ori
PGAL1
pYESHyg(x)eGFP

Figure 10